

8072

GAACAGATTTGGAATAACATGACCTGGA TGGAGTGGGACAGAGAAATTAA

GAAGAGATTTGGGAGAACATGACCTGGATGCAGTGGGAAAAGAAATTCA

GAAACAATTTGGGATAACATGACCTGGATCCACTGGGAAAGAGAAATTGA

GAAACAATTTGGGATAACATGACCTGGATGCAGTGGGAAAGAGAAATTGA

GAAATTAA

8121

CAATTACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAACCAGC

CAATCACACAAAATACATATACTCCTTACTTGAAAATCGCAGAACCAAC

CAATTACACAACATAATATACACCTTAATTGAAGAATCGCAGAACCAAC

CAATTACACAACATAATATACACCTTAATTGAAGAATCGCAGAACCAAC

CAATTACACAAGATTAATATACAACCTTAATTGAAGAATCGCAGAACCAAC

8171

FIGURE 1

00146783-090788

AAGAAAAGAATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTG

AAGAAAAGAATGAACAAGAACTATTGGAATTGGATCAATGGGCAAGTTTG

AAGAAAAAATGAAC TAGAATTATTGGAATTGGATAAATGGGCAAATTTG

AACAAAAAATGAAC TAGAATTATTGGAATTGGATAAATGGGCAAATTTG

AAGAAAAGAATGAACAAGACTTATTGGAATTAGATAAATGGGCAAGTTTG

8221

TGGAATTGGTTTAACATAACAAATTGGCTGTGGTATATAAAATTATTCAT

TGGAATTGGTTTGACATAACAAATGGCTGTGGTATATAAAATATTCAT

TGGAATTGGTTTAGTATATCAAACTGGCTATGGTATATAAAATTATTCAT

TGGAATTGGTTTAGTATATCAAACTGGCTATGGTATATAAAATTATTCAT

TGGAATTGGTTTGACATAACAAGTGGGCTGTGGTATATAAAATTATTCAT

8271

FIGURE 1

094633 000390

8321

SA10

8371

[illegible]

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Tat terminati n NL43

CACCTCCCAATCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGA 8421
*** **
CTCCTCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATCGAAGAAGA

CACCTCCCAACCCCGAAGGGACCCGACAGGCCAGAAGGAATCGAAGAAGA

CACCTCCCAACCCCGAGGGGACCCGACAGGCCAGAAGGAATCGAAGAAGA

CACCTCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATCGAAGAAGA

AGGTGGAGAGAGAGACAGAGACAGATCCATTGATTAGTGAACGGATCCT 8471

AGGTGGAGAGAGAGACAGAGACAGATCCACTCCATTACTACACCGATTCT

AGGTGGAGAGAGAGACAGAGGCAGCTCCACTCGATTAGTGCACGGATTCT

AGGTGGAGAGAGAGGCAGAGGCAGTCCACTCGATTAGTGCACGGATTCT

AGGTGGAGAGAGAGACAGAGACAGATCCAGTCGATTAGTGCACGGATTCT
D36P, C18S, C18M & C98H Tat termination

FIGURE 1

TAGCACTTATCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCTACCAC

TAGCACTTTTCTGGGACGACCTGAGGAGCCTGTGCCTCTTCCTCTACCAC

TAGCACTTTTCTGGGACGACCTGAGGAGTCTGTGCCTCTTCAGCTACCAC

TAGCACTTTTCTGGGTGACCTGAGGAGTCTGTGCCTCTTCAGCTACCAC

TAGCACTTTTCTGGGTGACCTGAGGAGCCTGTGCCTCTTCAGCTACCAC

8521

CGCTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTGGAACTTCTGGG
*
CACTTGAGAGACTTACTCTTGATTGTAACAAGGATTGTGGAACTTCTGGG
*
CACTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTGGAACTTCTGGG
*
CGCTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTGGAACTTCTGGG
*
CGCTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTGGAACTTCTGGG

8571

FIGURE 1

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ACGCAGGGGGTGGGAAGCCCTCAAATATTGGTGGAATCTCCTACAGTATT
** ***** **
ACGCAGGGGGATGGGAAGCCCTCAAATATTGGTGGAACCTCCTAAAGTATT
**** **
ACGCAGGGGGATGGGAAGCCCTCAAATACTGGTGGAATCTCCTGCAGTATT

ACGCGGGGGATGGGAAGCCCTCAAATACTGGTGGAATCTCCTGCAGTATT

ACGCAGGGGGTGGGAAGCCCTCAAATATTGGTGGAATCTCCTACAATATT

8621

NL43 Rev termination

GGAGTCAGGAACTAAAGAAATAGTGCTGTTAACTTGCTCAATGCCACAGCC

GGAGCCAGGAACTGCAGAAGAGTGCTGTTATCTTCCTCAATGCCACCGCC

GGAGGCAGGAACTACAGAAGAGTGCTGTTAGCTTGTTCAATGGCACGGCC

GGAGACAGGAACTACAGAAGAGTGCAAGTTAGCTTGTTCAATGCCATAGCC

GGAGTCAGGAACTCAAGAAGAGTGCTATTAGCTTGTTCAATGCCACCGCC

8671

C18S, C18M & C98H Rev termination

FIGURE 1

09146783 090398
090600 234750

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ATAGCAGTAGCTGAGGGGACAGATAGGGTTATAGAAGTATTACAAGCAGC
* * * * *

8721

ATAGCAGTAGCTGAGGGGACAGATAGAGTTTATAGAAGTATTACAAGAGC
* * * * *

ATAGCAGTAGCTGAGGGGACAGATAGAGTTATAGAAGCTTTACCAAGGGC
* * * * *

ATAGCAGTAGCTGAGGGGACAGATAGAGCTATAGAAGGATTACAAACACC
* * * * *

ATAGCAGTAGCTGAGGGGACAGATAGAGTTATAGAAGTATTACAAGAGC
* * * * *

incomplete . AGGGGACAGATAGAGTTCTAGAAGTATTACAAGAGC
D36P Rev termination

TTATAGAGCTATTCGCCACATACCTAGAAGAATAAGACAGGGGCTTGGAAA
* * * * *

8771

TTATAGAGCTATCCTCCACATACCTAGAAGAATAAGACAGGGCCTCGAAA
* * * * *

TTATAGAGCTATTCCTCCACATACCTAGAAGAATAAGACAGGGGCTTAGAAA
* * * * *

TTATAGAGCTATTCCTCCACATACCTAGAAGAATAAGACAGGGGCTTAGAAA
* * * * *

TTGTAGAGCTGTTCTCCACATACCTAGAAGAATAAGACAGGGGCTTCGAAA
* * * * *

TTATAGAGCCATTCTCCACATACCTAGAAGAATAAGACAGGGGCTTCGAAA

FIGURE 1

09146788 090399

FIGURE 1

9/101

GGGTGGGAGCAGTATCTCGAGACCTAGAAAAACATGGAGCAATCACAAGT
* * * * *

8921

GGGTGGGGGC-----

GGGTGGGAGCAATATCTCGAGACCTAGGAAAACATGGAGCAATCCCAAGT

GGGTGGGAGC-----

SIV_{mac239} IPTC

AGCAATACAGCAGCTAACAATGCTGCTTGTGCCTGGCTAGAAGCACAAGA
* * * * *

8971

-----CAACAACCTAACAATGCTGATCGTGCCTGGCTAGAAGCACAAGA

AGCAATACAACAACCTAACAATGCTAATTGTGCCTGGCTAGAAGCACAAGA
* * * * *

-----CAACAACCTAACAATTCTGGTTGCGCCTGGCTAGAAGCA-----

FIGURE 1

10/101

GGAGGAAGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAA

9021

GAAGGAAGAAGCGGGTTTTCCAGTCAAACCTCAGGTA-----

-----TACCTTTAAGAC--

GGAGGAGGAAGTGGGTTTTCCAGTCAAACCTCAGGTACCTTTAAGACCAA

Poly purine tract

TGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTTAAAGAAAAGGGG

9071

-----GCTGTAGATCTTAGCCACTTTTTTAAAGAAAAGGGG

-----AAGGCAGCTATAGATCTTAGCCGCTTTTTTAAAGAAAAGGGG

-----GATCTTAGCCACTTTTTTAAAGAAAAGGGG

TGACTTACAAG-----GCCACTTTTTTAAAGAAAAGGGG

-----CACTTTTTTAAAGAAAAGGGG

C18S nef termination

C18M and C98H nef Termination

FIGURE 1

11/101

[U3

GGACTGGAAGGGCTAATTCACCTCCCAAAGAAGACAAGATATCCTTGATCT

9121

GGACTGGAAGGGCTAATTCACCTCCCAAAGAAGACAAGATA-----

GGACTGGAAGGGCTAATTCACCTCACAGAGAAGA-----

GGACTGGAAGGGCTAATTCACCTCACAGAGAAGA-----

GGACTGGAAGGGCTAATTCACCTCCTAAAGAAGACAAGATATCCTTGATCT

GGACTGGAAGGGCTAATACGCTCCCAAAGAAGACAAGATATCCTTGATCT

SA12

GTGGATCTACCACACACAAGGCTACTTCCCTGATTGGCAGAACTACACAC

9171

TTGGATCTACCACACACAAGGCTACT-----

**** *****

GTGGGGCTACCACACACAAGGCTACTTCCCTGATTGGCAGAACGACACAC

FIGURE 1

09145703 030900Z

12/101



{...dyad symmetry...
{...NRT-1.....

{ NRE -->

CAGGGCCAGGGGTCAGATATCCACTGACCTTTGGATGGTGCTACAAGCTA

9221

-----CACAGTGCTGCAAACCTA

-----ATCCACTGACTTTTGG, TGGTGCTTCAAATTA

CAGGGCCAGGGACCAGATATCCACTGACCTTTGGATGGTGCTGCAAACGA

.....)

.....)

myb

NF-AT

GTACCAGTTGAGCCAGAT AAGGTAGAAGAGGCCAATAAAGGAGAGAACAC

9271

TACCAGTGGAGTCAGCGAAGATAGAAGAGGCCAATGGAGGAGAAAACCA

---TCAGTTGAACCAGAAGAAGATAGAAGAGGCCATGAAGAAGAAAACAA

---TCAGTTGAACCAGAAGAAGATGAAGAGGCCATGAAGAAGAAAACAA

GTACCAGTGGANCCAGA--AGAGAGAAGAGACCAATGGAGGAGAGAACA-

GTACCAGGGGAAACAGAGAAGATAGAAGAGGCCAATGGAGGAGAAAACAA

(myb)

FIGURE 1

9321

CAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGATGACCCTGAGAGAG
*** **

CAGATTGTT-----
*** **

CAGATTGTT-----
*** **

CAGATTGTT-----
*** **

*** **

CAGACTGTT-----

9371

<-- NRE]
 AAGTGTTAGAGTGGAGGTTTGACAGCCGCTAGCATTTATCACGTGGCC

 ----- CCGTTTGTT

 ----- CTGCT

 ----- A

FIGURE 1

14/101

TCF-1a

N f terminati n

CGAGAGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTA 9421
 * * * * *
 CTGTTGGGGACTTTCCATCCGTTGGGGACTTTCCAAGGCGGCGTGGCCTG
 * * * * *
 CCGTTGGGGACTTTCCA, , , , , GGAGACGTGGCCTGAGTGATAAGCCG
 * * * * *
 TGCTCAGCTGGGGACTTTCCAGAAGGCGCGGCCTGAGTGACTAAGCCCCG
 * * * * *
 CAGAGTGTGGGGACTCTCCACAACAGAGTGTGGGGACTTTCCAAGGAGGC
 * * * * *
 ----CCGTTGGGGACTTTCCAAGGAGGCGTGGCCTGAGTGACTAAGTTCC
 D36P, C18S, C18M & C98H extra NFkB
 D36P & C98H extra NFkB

| NFkB | NFkB | Sp1 | |
|---|------------------------------|-----------|------|
| CAAGGGACTTTCCG, , , , , | CTGGGGACTTTCCAG, GGAGGCGTGGC | | 9461 |
| * * * * * | * * * * * | * * * * * | |
| GGTGACTAGTTCCG, , , , , | GTGGGGACTTTCCAA, GAAGGCGCGGC | | |
| * * * * * | * * * * * | * * * * * | |
| CTGGGGACTTTCCGAAGAGGCGTGACGGGACTTTCCAA, GGCGACGTGGC | | | |
| * * * * * | * * * * * | * * * * * | |
| TTGGGACTTTCCGAAGAGGCATGAAGGGACTTTCCAAG, GCAGGCGTGGC | | | |
| * * * * * | * * * * * | * * * * * | |
| GTGGCCTGAGTGACTAAGTTCCGTTGGGGACTTTCCAA, AAAGGCGAGGC | | | |
| * * * * * | * * * * * | * * * * * | |
| GTTGGGACTTTCCAAGGAGGC, , GCGGGGACTTTCCAA, GGAGGCGCGGC | | | |
| C18S & C18M NFkB | NFkB | Sp1 | |
| D36P and C98H 3'-half NFkB | | | |

FIGURE 1

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Sp1

Sp1

TATA box

CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG
 * * * * *
 CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG
 * * * * *
 CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG
 * * * * *
 CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG
 * * * * *
 CTGGGCGGA-CTGGGGAGTGC-GAGCC-, TCAGATGCTGCATATAGGCAG
 * * * * *
 CTGGGCGGGACTGGGGAGGGGCGAGCCC, TCAGATGCTGCATATAAGCAG

9510

Sp1

Sp1

U3

R

TAR

CTGCTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG
 * * * * *
 CTGCTTTCTGCTGTTACTGGGTCTCTCGGGTTAGACCAGATCTGAGCCTG
 * * * * *
 CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG
 * * * * *
 CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG
 * * * * *
 CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG
 * * * * *
 CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG
 * * * * *

9560

CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCT...incomplete

FIGURE 1

09146783-00398

001463-0000

16

17/101

AACTAGAGATCCCTCAGACCCTTTTAGTCAGTGTGGAAAATCTCTAGCA 9709

* *****

ATCTAGA 1305

* *****

ATCTAGA 1209

* *****

ATCTAGAGATCCCTCAGACCATTTTAGTCCGTGTGGAAAATCTCTAGCA END

* *****

ATCTAGA 1399

00446783-100398

FIGURE 1

FIGURE 2

| |
|--------|
| 19/101 |
| 20/101 |

19/101

FIGURE 2A

86

PTSQSRGDP TGPKE#

NL43 73

635

PSSQPRGDP TGPKEKKKVERETETDPLD#

D36P BMC

636

PTSQPRRDPTGQESKKKVERETEAAPLD#

C18 HIV_{scv}

637

PTSQPRRDPTGQESKKKVERETEAAPLD#

C18 HIV_{MBC}

C98 HIV

PTSQPRRDPTGQESKKKVERETETDPVD#

FIGURE 2B

65

DPPNPEGTRQARRNRRRRWRERQRQIHSISERILSTYLG

NL43 26

638

DPPNPEGTRQARRNRRRRWRERQRQIHSISTRILSTFLG

D36P BMC

639

DPPNPEGTRQARRNRRRRWRERQRQLHSISARILSTFLG

C18 HIV_{stv}

640

DPPNPEGTRQARRNRRRRWRERQRQLHSISARILSTFLG

C18 HIV_{MBC}

DPPNPEGTRQARRNRRRRWRERQRQIQISARILSTFLG

C98 HIV

20/101

FIGURE 2B

NL43 RSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVE 105

D36 PBMC RPEEPVPLPLPPLERLTLDNCNKDCGTSGTQGMGSPQILVE

C18 HIV_{stv} RPEESVPLQLPPLERLTLDNCNEDCGTSGTQGMGSPQILVE

C18 HIV_{mbc} RPEESVPLQLPPLERLTLDNCNEDCGTSGTQGMGSPQILVE

C98 HIV RPEEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVE

NL43 SPTVLESGTKE#

D36PBMC PPKVLEPGTAEECCYLAQCHRHSSS#

C18 HIV_{stv} SPAVLEAGTTEBCC#

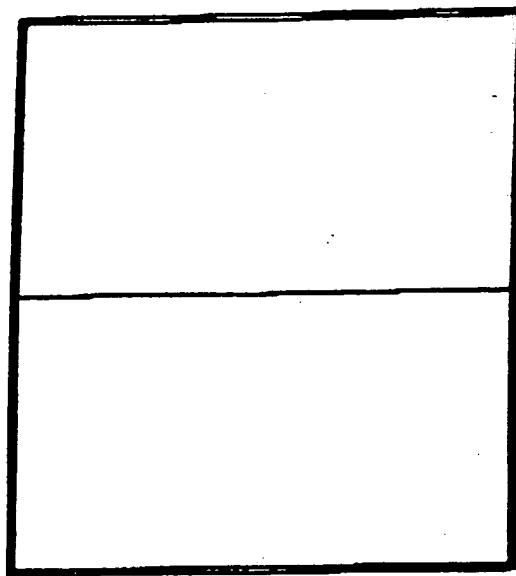
C18 HIV_{mbc} SPAVLEAGTTEBCC#

C98 HIV SPTILESGTQEECCY#

116

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FIGURE 3



00146783-003388
000000-000000

FIGURE 3

611 NL43 EQIWNNTMWDREINNNTSLIHSLEESQSQKNEQELLELDKWASL 639
 612 D36P BMC BEIWENMTMQWEKEIHNTKYIYSLLEKSQSQKNEQELLELDQWASL
 613 C18 HIV^{Stv} ETIWDNMTMQWEREIDNYTNIITYLLEESQSQKNELELELDKWANL
 C18 HIV^{MBC}
 C98 HIV EINNYTRTIYNLIEESQSQKNEQDLELDKWASL

2/101

689
 NL43 WNWENITNWLWYIKLFIMVGGVLGLRIVFAVLSIVNRVRQGYSPLSFQT
 D36 BMC WNWFDITKWLWYIKLFIMVGGVLGLRIVFAVLSIVNRVRQGYSPLSFQT
 C18 HIV^{Stv} WNWFSISNWLWYIKLFIMVGGVLGLRIVFTVLSIVNRVRQGYSPLSFQT
 C18 HIV^{MBC}
 C98 HIV WNWFDITSGWLWYIKLFIMVGGVLGLRIVLAVLSIVNRVRQGYSPLSFQT

FIGURE 3

NL43 739

HLPIPRGPDPRPEGIEEGGERDRDRSIRLVNGSLALINDDLRSLCLFSYH

D36 PBMC

LLPTPRGPDPRPEGIEEGGERDRDRSTRLVHGFLALFWDDLRSLCLFLYH

C18 HIV_{stv}

HLPTPKGPDPRPEGIEEGGERDRGSSTRLVHGFLALFWDDLRSLCLFSYH

C18 HIV_{mbc}

C98 HIV

HLPTPRGPDPRPEGIEEGGERDRDRSSRLVHGFLALFWVDLRSLCLFSYH

NL43 789

RLRDLLLVTRIVELLGRRGWEALKYWNLLQYWSQELKNSAVNLLNATA

D36 PBMC

HLRDLLLVTRIVELLGRRGWEALKYWNLLKYWSQELQKSAVILLNATA

C18 HIV_{stv}

HLRDLLLVTRIVELLGRRGWEALKYWNLLQYWRQELQKSAVSLFNGTA

C18 HIV_{mbc}

C98 HIV

RLRDLLLVTRIVELLGRRGWEALKYWNLLQYWSQELKKSAISLFNATA

NL43 839

IAVAEGTDRVIEVLQAAAYRAIRHIPRIRQGLERILL#

D36 PBMC

IAVAEGTDRVIEVLQRAYRAIRHIPRIRQGLEMALL#

C18 HIV_{stv}

IAVAEGTDRVIEALRAYRAIRHIPRIRQGLERALL#

C18 HIV_{mbc}

IAVAEGTDRVIEVLQACRAVLHIPRIRQGFERAML#

C98 HIV

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FIGURE 4

| | | |
|-------------------------|--|-----|
| NL43 | MGGKWSKSSVIGWPAVRRMRRAEPAADGVGAVSRDLEKHGAITSNTAA *** | 50 |
| D36 P BMC | MGGK# ***** | 4 |
| C18. HIV _{Stv} | MGGKWSKSSVRRHVPLRQGSYRS# * | 24 |
| C18 HIV _{WBC} | MRILATF# ***** | 7 |
| C98 HIV | MGGKWLKSSMVRWPAVREKMKQAEPAABGVGAISRDLGKHGAIPSSNTTT | 50 |
| NL43 | NNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGL *** | 100 |
| C98 HIV | NNANCANLEAQEEEEVGFPVKPQVPLRPMTYKATF# | 85 |
| NL43 | IHSQRRQDILDLIWYHTQGYFPDQNYTPGPGVRYPLTFGWCYKLVPEP | 150 |
| NL43 | DKVEBANKGENTSLLHPVSLHGMDPPEREVLEWRFDLSRLAFHHVARELHP | 200 |
| NL43 | BYFKNC* | 206 |

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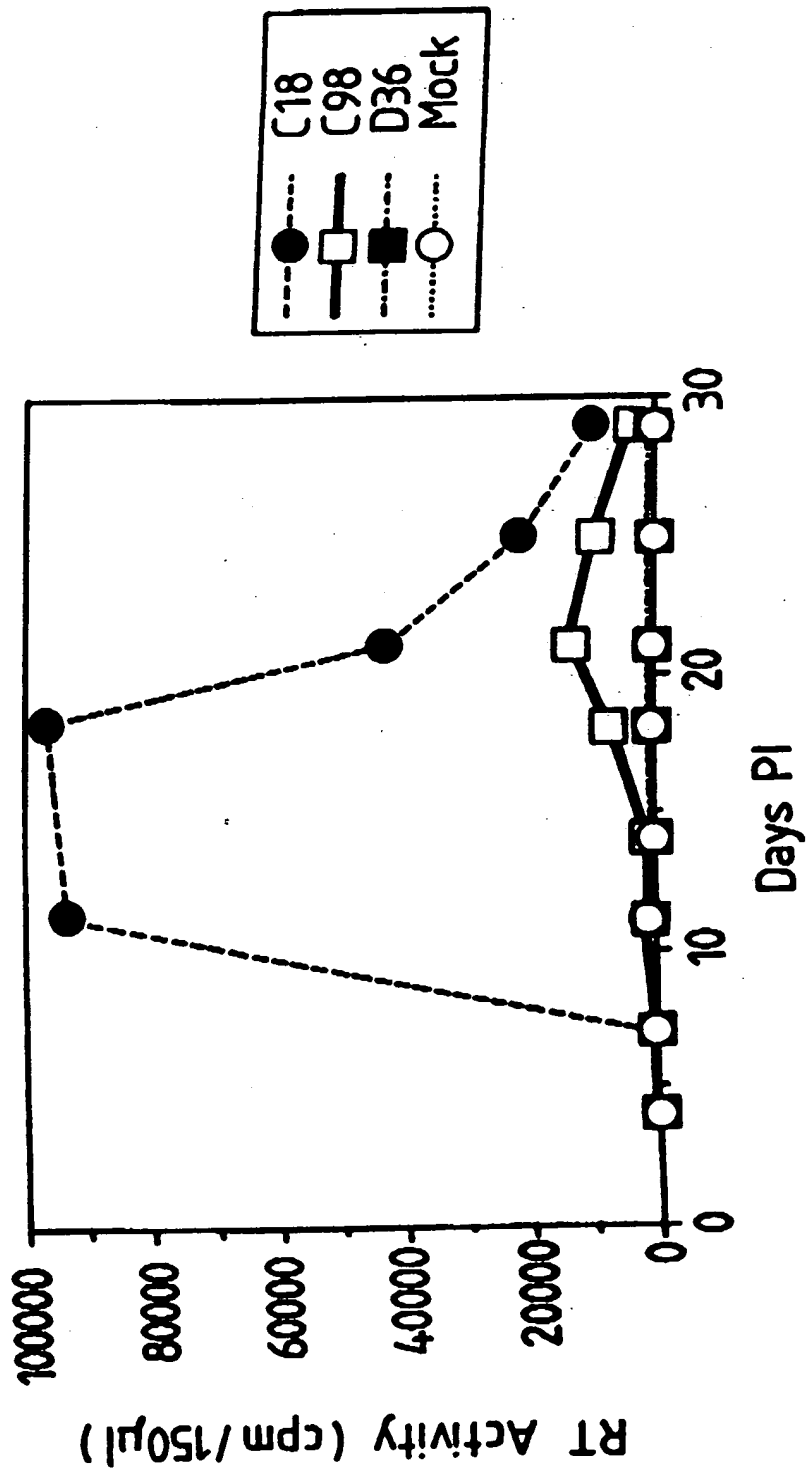
FIGURE 5

| | NFkB | NFkB |
|------------------------|---|---------------|
| 9419 NL43 | CGAGCTTGCTACAAGGGACTTTCC, , , , GCTGGGACTTTCCAGGGA ***** | ***** |
| D36 PBMC | ACTGTTGGGGACTTTCCATCCGTTGGGGACTTTCCAGGC ***** | ***** |
| C18 HIV _{stc} | ACCGTTGTTCGTTGGGGACTTTCCA-GGA ***** | ***** |
| C18 HIV _{mbc} | ACTGCTTGCTCAGCTGGGGACTTTCCA-GAA ***** | ***** |
| C98 HIV | ΔACAGAGTGTGGGACTCTCCACACAGAGTGTGGGGACTTTCCAGGA ***** | ***** |
| C54 PBMC | ΔCCGTTGGGGACTTTCCAGGA ***** | ***** |
| | NFkB | NFkB |
| | Sp1 | Sp1 |
| NL43 | GGCGTGGCCTGGGGGACTGGGGAGTGGCG-AGCCCTCA ***** | 9492 ***** |
| DC36 PBMC | GGCGTGGCCTGGGTGACTAGTTCGGTGGG-ACTTTCCA ***** | ***** |
| C18 HIV _{stc} | GACGTGGCCTGAGTGACTAAG-CGGCTGGG-ACTTTCCG ***** | ***** |
| C18 HIV _{mbc} | GGCGGGCCTGAGTGACTAAGCCCGTTGG-ACTTTCCG ***** | ***** |
| C98 HIV | GGCGTGGCCTGAGTGACTAAGTTCGGTGGGACTTTCCA ***** | ***** |
| C54 PBMC | GGCGTGGCCTGAGTGACTAAGTTCGGTGGGACTTTCCA Sp1 3' half NFkB | NFkB |

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FIG 6

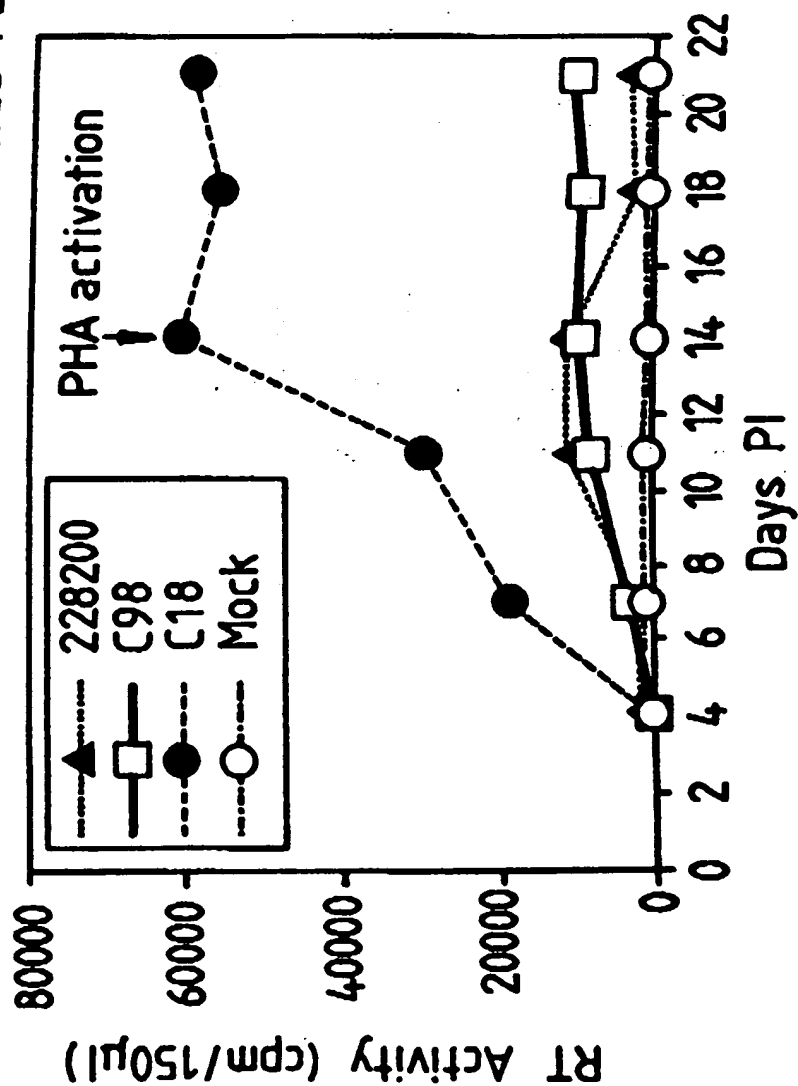
**Replication of Sydney Asymptomatic
Patients Isolates in PHA-stimulated PBMCs**



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FIG 7

Replication of Sydney Asymptomatic
Patient Isolates in non-PHA stimulated PBMCs



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FIG 8

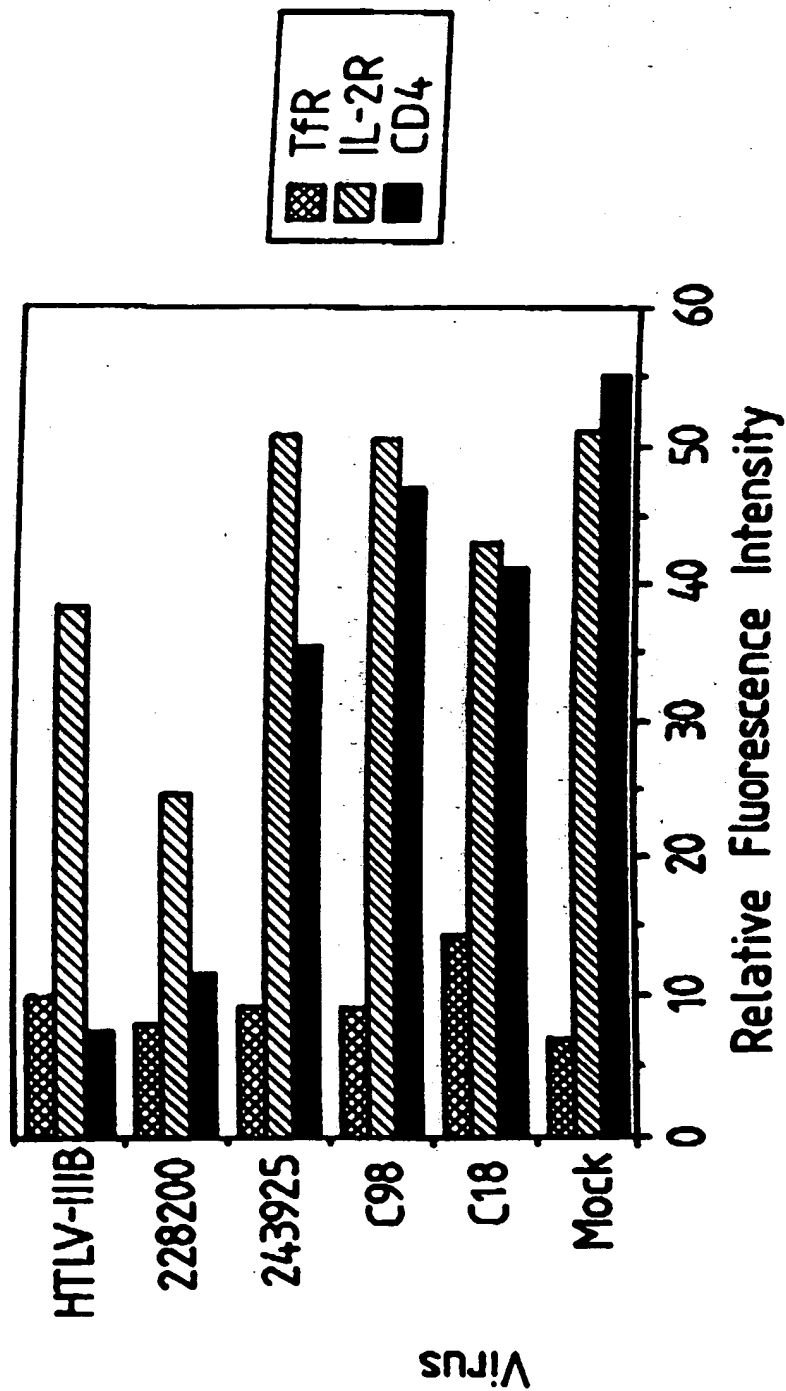




FIGURE 9

SECRET

SECRET

TGGAAGGGCTAATTCACCTCACGGAAAAGACCAGTTGAACCAG
AAGAAGATAGAAGAGGCCATGAAGAAGAAAACAACAGATTGT
TCTGCTTGCTCAGCTGGGGACTTTCCAGAAGGCGCGGCCTGA
GTGACTAAGCCCCGTTGGGGACTTTCCGAAGAGGCATGAAGG
GACTTTCCAAGGCAGGCGTGGCCTGGGCGGGACTGGGGAGTG
GCGAGCCCTCAGATGCTGCATATAAGCAGCTGCTTTCTGCCT
GTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGC
TCTCTGGCTAGCTAGGGAACCCACTGCTTAAGCCTCAATAAA
GCTTGCCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGT
GTGACTCTGGTATCTAGAGATCCCTCAGACCATTTTAGTCCG
TGTGGAAAATCTCTAGCAGTGGCGCCCCGAACAGGGGACTTGAA
AGCGAAAGGAAAACCAGAGGAGCTCTCTCGACGCAGGACTCG
GCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACT
GGTGAGTACGCCGAAAATTTTGACTAGCGGAGGCTAGAAGGA
GAGAGATGGGTGCGAGAGCGTCAATATTAAGCGGGGGAATA
TAGATAGATGGGAGAAAATTCGGTTAAGGCCAGGAGGAAAGA
AAAAGTATAAATTAAACATATAGTATGGGCAAGCAGGGAGC
TAGAACGATTTCGCAGTCAATCCTGGCCTGTTGGAAACATCAG
AAGGCTGTAGACAAATACTGGGACAGTTACACCCGTCCCTTC
AGACAGGATCAGAAGAACTTAAATCAGTATATAATGCAGTAG
CAGTCCTCTATTGTGTGCATCAAAACATAGACATAAAGGACA
CCAAGGAAGCTTTAGAAAAGATAGAGGAAGAGCAAAACAAAT
GTAAGAAAAAAGCACAGCAAGCAGCAGCACAGCAAGCAGCAG
CTGGCACAGGAAACAGCAACCCGGTCAGCCAAAATTACCCTA
TAGTACAGAACATGCAGGGGCAAATGGTACATCAGGCCATAT
CACCTAGAACTTTAAATGCATGGGTAAAAGTAATAGAAGAGA
AGGCTTTTCAGCCCAGAGGTAATACCCATGTTTTTCAGCATTAT
CAGAAGGAGCCACCCACAAGATTTAAACACCATGCTAAACA
CAGTGGGGGGACATCAAGCAGCTATGCAAATGTTAAAAGAGA
CCATCAATGAGGAAGCTGCAGAATGGGATAGATTACATCCAG
CGCAGGCAGGGCCTGTTGCACCAGGCCAGATGAGAGACCCAA
GGGGAAGTGACATAGCAGGAACTACTAGTACCCTTCAGGAAC
AAATAGGATGGATGACAGGTAATCCAGCTATCCCAGTAGGAG
AAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAG
TAAGGATGTATAGCCCTATCAGCATTCTGGACATAAAACAAG
GACCAAAGGAACCCTTTAGAGACTATGTAGACCGGTTCTATA
AACTCTAAGAGCCGAGCAAGCTACACAGGAGGTAAAAAATT
GGATGACAGAAACCTTGTTGGTCCAAAATGCAAACCCAGATT
GTAAGACTATTTTAAAAGCATTGGGACCAGCAGCTACACTAG

AAGAAATGATGACAGCATGTCAGGGAGTGGGAGGACCCAGCC
ATAAAGCAAGAGTTTTTGGCAGAAGCAATGAGCCAAGCAACAA
ATGCAGCTACTGTAATGATGCAGAGAAGCAATTTTAGAAACC
AAAGAAAGAATGTTAAGTGTTTCAATTGTGGCAAAGAAGGGC
ACATAGCCAGAAATTGCAGGGCTCCTAGGAAAAGGGGGCTGTT
GGAAATGTGGAAAGGAAGGACACCAAATGAAAGATTGTACTG
AGAGACAGGCTAATTTTTTTAGGGAAAATCTGGCCTTCCCACA
AGGGGAGGCCAGGGAACTTTCTTCAGAGCAGGCCAGAACCAA
CAGCCCCCTCTCCAGGGCAGGCCGGAGCCATCAGCCCCGCCAG
AAGAGAGCTTCAGGTTTGGGGAGGAGACAACAACCTCCCTCTC
AGAAGCAGGAGCCGATAGACAGGGACAGGGATCTGTATCCTT
TAGCTTCCCTCAGATCACTCTTTGGCAACGACCCCTCGTCAC
AATAAAGATAGGGGGGCAGCTGAAGGAAGCTCTATTAGATAC
AGGAGCAGATGATACAGTATTAGAAGACATGCATTTGCCAGG
AAAATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTAT
CAAAGTAAAACAATATGATGAAATTCTTGTAGAAATCTGTGG
ACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGT
CAACATAATTGGAAGAAATCTGTTGACTCAGATTGGTTGCAC
TTTAAATTTTCCCATTAGTCCTATTGAAACTGTACCAGTACA
ATTAAAGCCAGGAATGGATGGCCCAAAGGTTAAACAATGGCC
ATTGACAGAAGAGAAAATAAAAGCATTAGTAGAAATTTGTAC
AGAAATGGAAAAGGAAGGAAAGATTTCAAAAATTGGGCCTGA
AAATCCATACAATACTCCAGTATTTGCCATAAAGAAAAAAGA
TGGTACTAAATGGAGAAAATTAGTAGATTTAGAGACCTTAA
TAAGAGAACTCAAGACTTCTGGGAAGTTCAATTAGGAATACC
ACATCCCTCAGGATTAAGAAAAGAAAAAATCAGTAACAGTACT
GGATGTGGGTGATGCATACTTTTCAGTTCCCTTAGATGAAAA
CTTCAGGAAGTATACTGCATTTACCATACCTAGTATAAATAA
TGAGACACCAGGGATTAGATATCAGTACAATGTGCTTCCACA
GGGATGGAAAGGATCACCAGCAATATTCCAAAGTAGCATGAC
AAGAATCTTAGAGCCTTTTAGAAGACAAAATCCAGACATAGT
TATCTATCAATACATGGATGACTTGTATGTAGGATCTGATTT
AGAAATAGGACAGCATAGAATAAAAAATAGAGGAACTGAGACA
ACATCTGTTGAAGTGGGGATTTACCACACCAGACAAAAAGCA
TCAGAAAGAACCCCCATTCTTTGGATGGGTTATGAACTCCA
TCCTGATAAATGGACAGTGCAACCTATAGTACTGCCAGAAAA
AGACAGCTGGACTGTCAATGACATACAGAAGTTAGTGGGTAA
ATTAAATTGGGCAAGTCAGATTTACCCAGGAATTAAAGTAAG
GCAATTATGTAAACTCCTTAGGGGAACCAAAGCACTAACAGA

FIGURE 9

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AGTAATACCACTAACAGAAGAAGCAGAGCTAGAACTGGCAGA
AAACAGGGAAATTCTAAGAGAACCAGTACATGGAGTGTATTA
TGACCCATCAAAAGACTTAATAGCAGAAATACAGAAGCAGGA
GCAAGGCCAATGGACATATCAAATTTATCAAGATCAATTTAA
AAATCTAAAAACAGGAAAGTATGCAAGATTGAGGGGTGCCCA
CACTAATGATGTAAAACAATTTCCAGAGGCAGTGCAAAAAAT
AGCCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATT
TAGACTACCCATACAAAAAGAAACATGGGACGCATGGTGGAC
AGAGTATTGGCAAGCCACCTGGATTCTGAGTGGGAGTTTGT
CAATACCCCTCCCCTAGTAAAATTATGGTACCAGTTAGAAAA
AGAACCCATAATAGGAGCAGAACTTTCTATGTAGATGGGGC
AGCTAACAGAGAGACTAAATTAGGAAAAGCAGGATATGTTAC
TGACAGAGGAAGACAAAAAGTTGTCTCCCTAACTGACACAAC
AAATCAGAAGACTGAGTTACAAGCAATTCATCTAGCTTTGCA
GGATTCAGGATTAGAAGTAAACATAGTAACAGACTCACAGTA
TGCATTAGGAATCATTCAAGCACACCAGATAAAAGTGAATC
AGAAATAGTCAATCAAATAATAGAGCAATTAATAAAAAAGGA
AAAGGTCTACCTGGCATGGGTACCAGCACACAAAGGAATTGG
AGGGAATGAACAAGTAGATAAATTAGTCAGTGCTGGAATCAG
GAAAATACTATTTTTAGATGGAATAGATAAGGCACAAGAAGG
CCATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAGTGG
TTTTAACCTGCCACCTATAGTAGCAAAAGAAATAGTAGCCAG
CTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACA
AGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACA
TCTAGAAGGAAAAATTATCCTGGTAGCAGTTCATGTAGCCAG
TGGATATATAGAAGCAGAAGTTATTCCAGCAGAGACAGGGCA
GGAAACAGCATACTTTATCTTAAAATTAGCAGGAAGGTGGCC
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TACCACGGTTAAGGCCGCCTGTTGGTGGGCAGGGATCAAGCA
GGAATTTGGCATTCCCTACAATCCCCAAAGCCAAGGAGTAGT
GGAATCTATGAATAGAGAATTAAAGAAAATTATAGGACAGGT
AAGAGATCAGGCTGAACATCTTAAGACAGCAGTACAAATGGC
AGTATTCATCCACAATTTTAAAAGAAAAGGGGGGATTGGGGG
ATACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGA
CATACAACTAAAGAATTACAAAAGCAAATTACAAAAATTCA
AAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCACTTTG
GAAAGGACCAGCAAACTTCTCTGGAAAGGCCGAAGGGGCAGT
AGTAATACAAGATAATAGTGACATAAAAGTAGTGCCAAGAAG
AAAAGTAAAGATCATTAGGGATTATGGAAAACAGATGGCAGG

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TGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAACAT
GGAACAGTTT TAGTGAAACACCATATGTATGTTTCAAAGAAAG
CTAAGGGATGGATTTATAGACATCACTATGAAAACACTCATC
CAAAAATAAGCTCAGAAGTACACATCCCAGTGGGGAAGCTA
GATTGGTAATAACAACATATTGGGGTCTACATACAGGAGAAA
GAGACTGGCATT TGGGTCAGGGAGTCTCCATAGAATGGAGGG
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AACTAATTCATATACATTACTTTGATTGTTTTTCAGAATCTG
CCATAAGAAGTGCCATATTAGGATATAGAGTTAGGCATAGGT
GTGAATATCAAGCAGGACATAACAAGGTAGGATCTCTACAGT
ACTTGGCACTAACAGCATT AATAACACCAAAGAAGATAAAGC
CACCTTTGCCTAGTGTTGCGAACTGACAGAGGATAGATGGA
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TGAATGGACACTAGAACTTTTAGAGGAGCTTAAGAATGAAGC
TGTTAGGCATTTTCCTAGGGTATGGCTCCATGGCTTAGGGCA
ACATATCTATGAACTTATGGGGATACTTGGGAAGGAGTGGA
GGCCATAACAAGAACTCTGCAACA ACTGCTGTTTATTCAATT
CAGAATTGGGTGTCAACATAGCAGAATAGGCATTATTGACA
GAGGAGAGCAAGAAATGGAGCCAGTAGATCCTAGACTAGAGC
CCTGGAAGCATCCAGGAAGTCAGCCTAAGACTGCGTGTACCA
CTTGCTATTGTAAAAAGTGCTGCTTTCATTGCCAAGTTTGTT
TTATGACAAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGC
GGAGACAGCGACGAAGAGCTCCTCAAGACAGTCAGACTCATC
AAGCTTATCTATCAAAGCAGTAAGTAATATATGTAATGCAAC
CTTTACAAATAGTAGCAATAGTAGCATTAGTAGTAGCAGGAA
TAATAGCAATAGTTGTGTGGACCATAGTATTCATAGAATATA
AGAAAATATTAAGACAAAGAAAAATAGACAGGTTGATTGATA
GAATAAGAGAAAGAGCAGAAGACAGTGGCAATGACAGTGAAG
GGGATCAGGAAGAATTATCGGCACTTGTGGACATGGGGCACC
ATGATCCTTGGGATATTAATGATCTGTAGAGCTGCAAACAAT
TTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAA
GCAACCACCACTCTATTTTGTGCATCAGATGCCAAGGCATAT
GATGCAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTA
CCCACAGACCCTAACCACACAAGAAGTAGAATTGAAAAATGTG
ACAGAAAATTTTAACATGTGGAAAAATAACATGGTAGAACAG
ATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTGAAG
CCATGTGTAAAATTAACCCCACTCTGTGTTTCTTTAAATTGC
ACTGATGCTACTAATACCACTAATAGTAATACCACTAGCAGC
AGCGAGAAACCGAAGGGGACAGGGGAAATAAAAAACTGCTCT

FIGURE 9

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TTCAATATCACCACAAGCATAAGAGATAAGGTGCAGAAACAA
TATGCACTTTTTTTATAGCCTTGATGTAGTACCAATGGATGAT
AATGATAATAGTACAAGCTATAGGTTAATAAGTTGTAACACC
TCAATCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCA
ATTCCCATAACATTATTGTGCCCGGCTGGTTTTGCGATTCTA
AAGTGTAAGATAAAAGGTTCAATGGAAAAGGACCATGTACA
AGTGTCAGCACAGTACAGTGTACACATGGAATTAGGCCAGTA
GTATCAACTCAACTGTTGTTAAATGGCAGTCTAGCAGAAGAA
GAGGTAGTAATTAGATCTGACAATTTTACGAACAATGCTAAA
ACCATAATAGTACAGCTGAGCAAATCTGTAGAAATTACTTGT
GTAAGACCCCAACAACAATACAAGAAAAAGTATAAGTATGGGA
CCAGGGAGAGCATTTTATACAACAGAAATAATAGGAGATATA
AGACAAGCATATTGTAACATTAGTAAAGCAAAGTGGACTGAC
ACTTTAGAACAGATAGCTAGAAAATTAAGAGAACAATTTGAG
AATAAAACAATAGTCTTTAAGCCATCCTCAGGAGGGGACCCA
GAAATTGTAACACAGTTTTTACAGTTTTTAATTGTGGAGGGGAA
TTTTTCTACTGTAATTCAACACAAGTGTTTAATGGTACTTGG
AATGGTACTTGGGTTAATGGTACTTGGAGTAGTAATAATACG
ACTGATACTGCAAATATCACACTCCCATGCAGAATAAAACAA
TTTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCC
CCTCCCATCAAAGGACAAATTAATGTACATCAATATTACA
GGGCTGATATTAACAAGAGATGGTGGTAACAATAACACCACG
AACGACAACGAGACCGAGACCTTCAGACCTGGAGGAGGAGAT
ATGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTA
GTACAAGTTGAACCATTAGGAGTAGCACCCACCAAGGCAAAG
AGAAGAGTGGTGCAAAGAGAGAAAAAGAGCAGTGGGAATAGGA
GCTATGTTCCCTTGGGTTCTTAGGAGCAGCAGGAAGCACTATG
GGCGCAGCGTCAGTGACGCTGACGGTACAAGCCAGACAATTA
TTGTCTGGTATAGTGCAGCAGCAGAACAATCTGCTGAGGGCT
ATTGAGGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGGC
ATCAAACAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGATAC
CTAAGGGATCAACAGCTCCTGGGACTTTGGGGTTGCTCTGGA
AACTCATTTCACCACTACTGTGCCTTGGAACAATAGCTGG
AGTAATAAATCTCTGGAAACAATTTGGGATAACATGACCTGG
ATGCAGTGGGAAAGAGAAATTGACAATTACACAAACATAATA
TACACCTTAATTGAAGAATCGCAGAACCAACAAGAAAAAAT
GAACTAGAATTATTGGAATTGGATAAATGGGCAAATTTGTGG
AATTGGTTTAGTATATCAAAGTGGCTATGGTATATAAAATTA
TTCATAATGGTAGTAGGAGGCTTGGTAGGTTTAAGAATAGTT

FIGURE 9

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TTTACTGTACTTTCTATAGTTAATAGAGTTAGGCAGGGATAC
TCACCATTATCGTTTCAGACCCACCTCCCAACCCCGAAGGGA
CCCGACAGGCCAGAAGGAATCGAAGAAGAAGGTGGAGAGAGA
GACAGAGGCAGCTCCACTCGATTAGTGCACGGATTCTTAGCA
CTTTTCTGGGACGACCTGAGGAGTCTGTGCCTCTTCAGCTAC
CACCACCTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTG
GAACTTCTGGGACGCAGGGGATGGGAAGCCCTCAAATACTGG
TGGAATCTCCTGCAGTATTGGAGGCAGGAACTACAGAAGAGT
GCTGTTAGCTTGTTCAATGGCACGGCCATAGCAGTAGCTGAG
GGGACAGATAGAGTTATAGAAGCTTTACGAAGGGCTTATAGA
GCTATTCTCCACATACCTAGAAGAATAAGACAGGGGCTTAGAA
AGGGCTTTGCTATAAAATGGGTGGCAAGTGGTCAGAAAGTAG
TGTGGTTAGAAGGCATGTACCTTTAAGACAAGGCAGCTATAG
ATCTTAGCCGCTTTTTTAAAGAAAAGGGGGGACTGGAAGGGC
TAATTCCTCACGGAAAAGACCAGTTGAACCAGAAGAAGATA
GAAGAGGCCATGAAGAAGAAAACAACAGATTGTTCTGCTTGC
TCAGCTGGGGACTTTCCAGAAGGCGCGGCCTGAGTGACTAAG
CCCCGTTGGGGACTTTCCGAAGAGGCATGAAGGGACTTTCCA
AGGCAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCCCT
CAGATGCTGCATATAAGCAGCTGCTTTCTGCCTGTACTGGGT
CTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCT
AGCTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTT
GAGTGCTTCAAGTAGTGTGTGCCCCGTCTGTTGTGTGACTCTG
GTATCTAGAGATCCCTCAGACCATTTTAGTCCGTGTGGAAAA
TCTCTAGCA

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trends in CD3 count since seroconversion

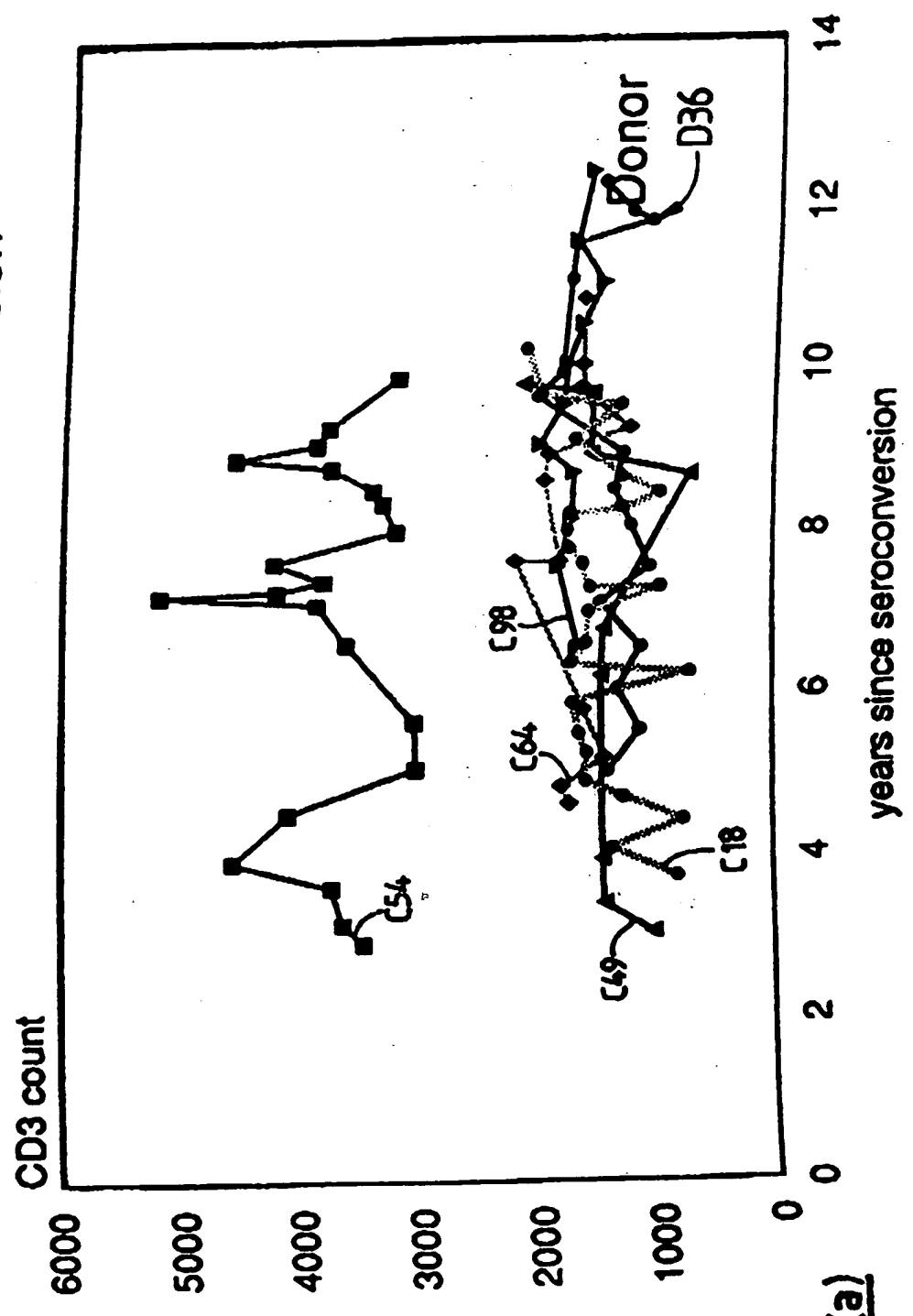
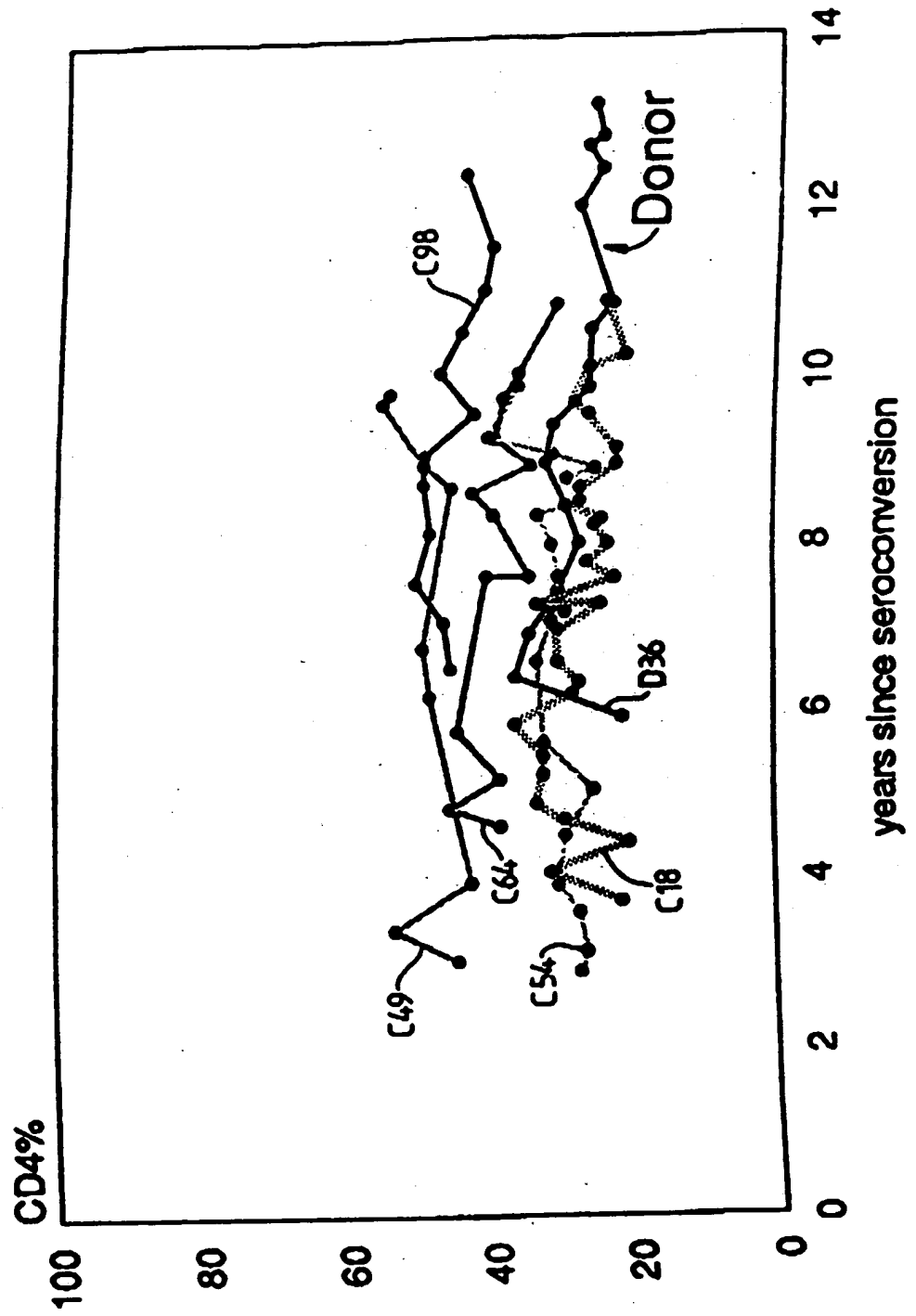


FIG 10(a)

FIG 10(b)(ii) trends in CD4% since seroconversion



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FIG 10(c)(i) trends in CD8 since seroconversion

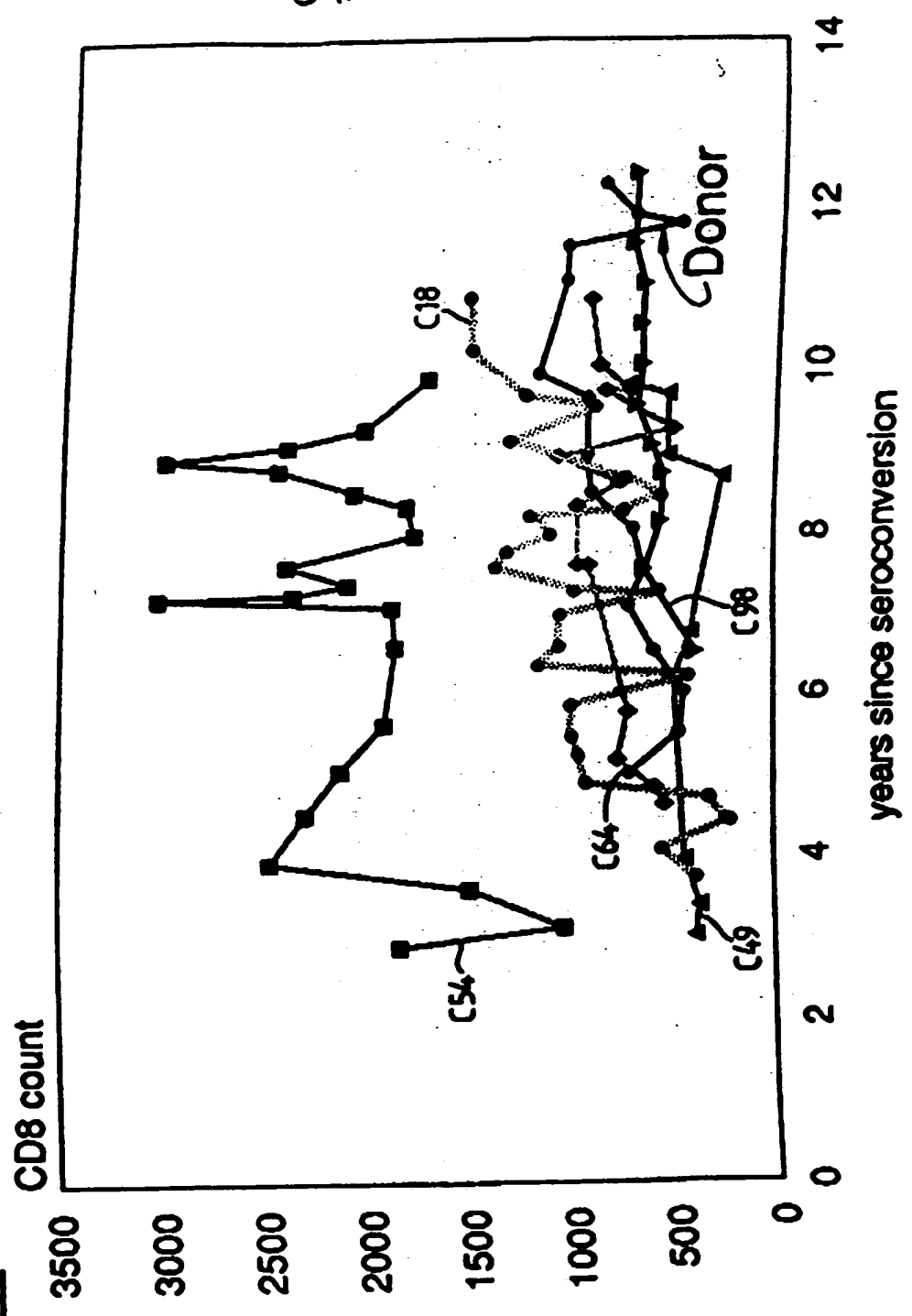
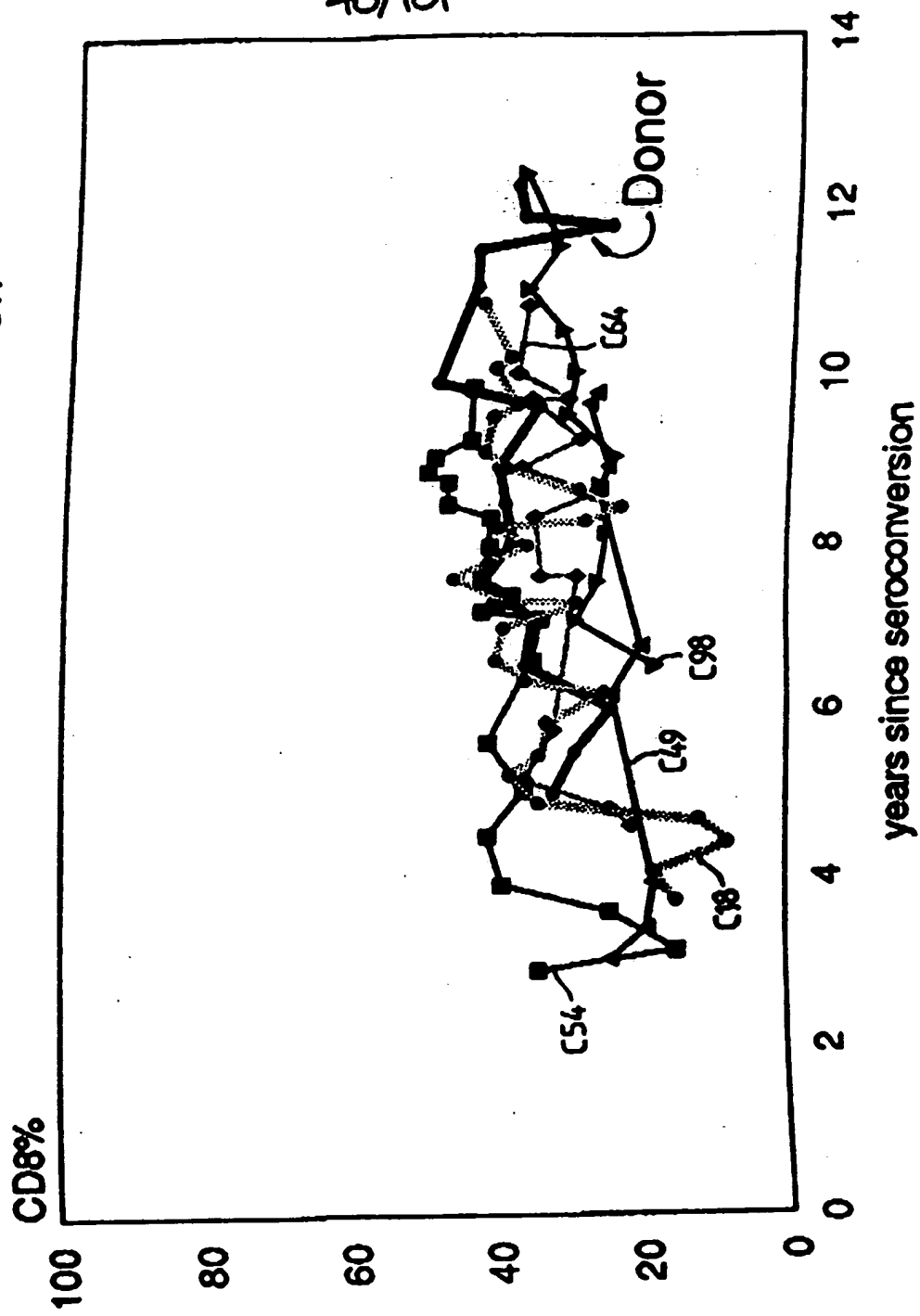


FIG 10(c)(ii)



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FIG 10 (d) trends in lymphocyte count since seroconversion

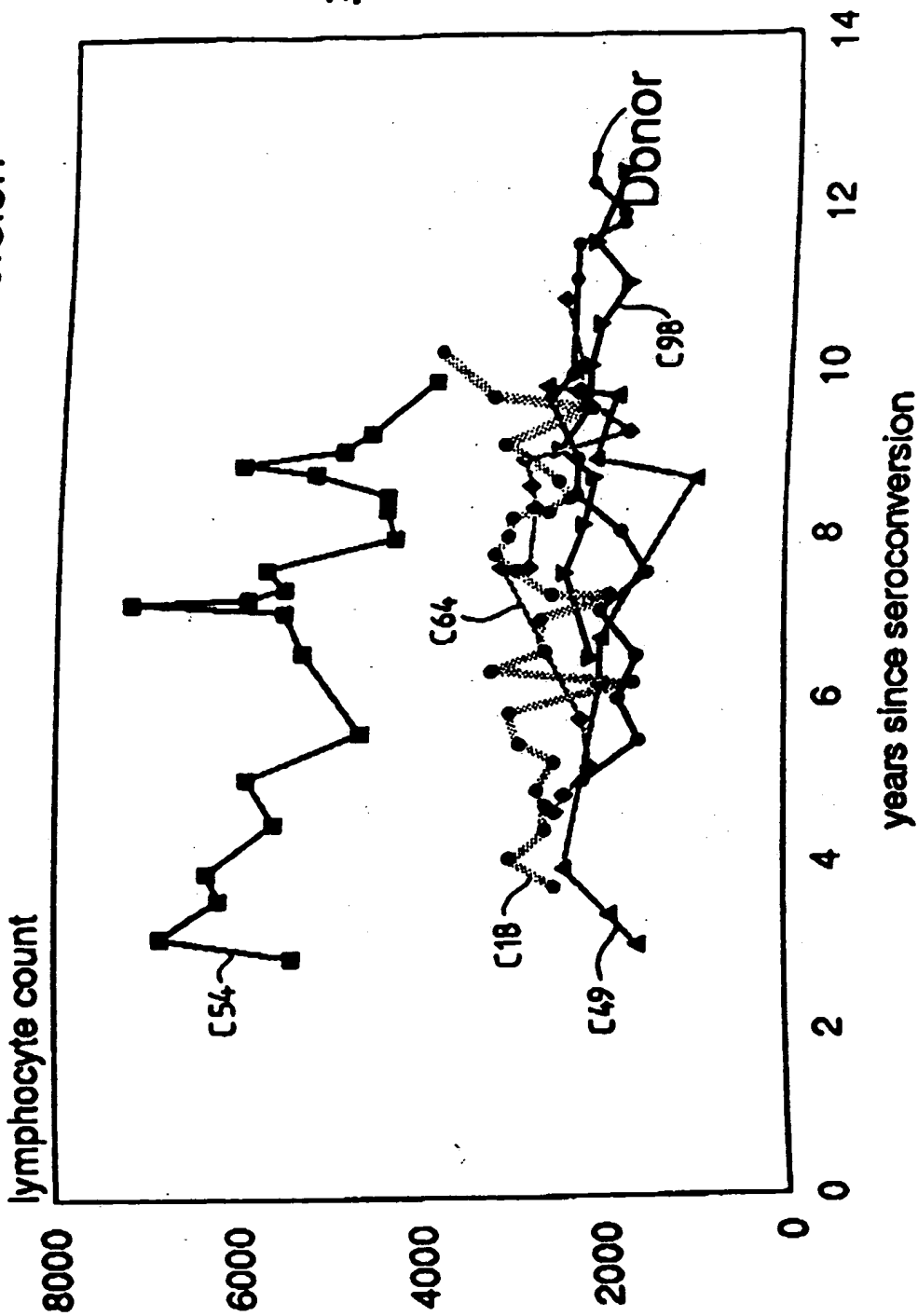
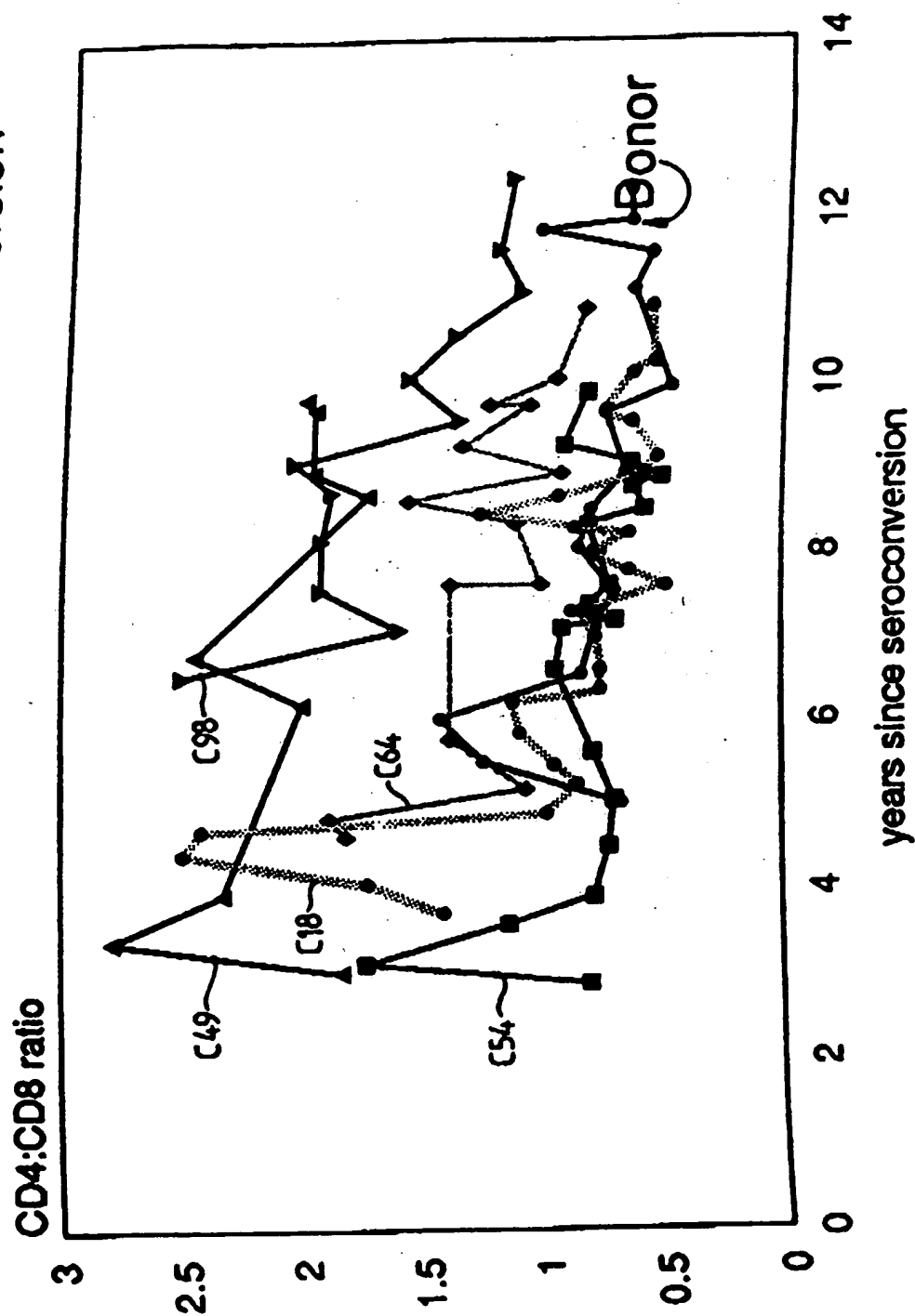


FIG 10(e)

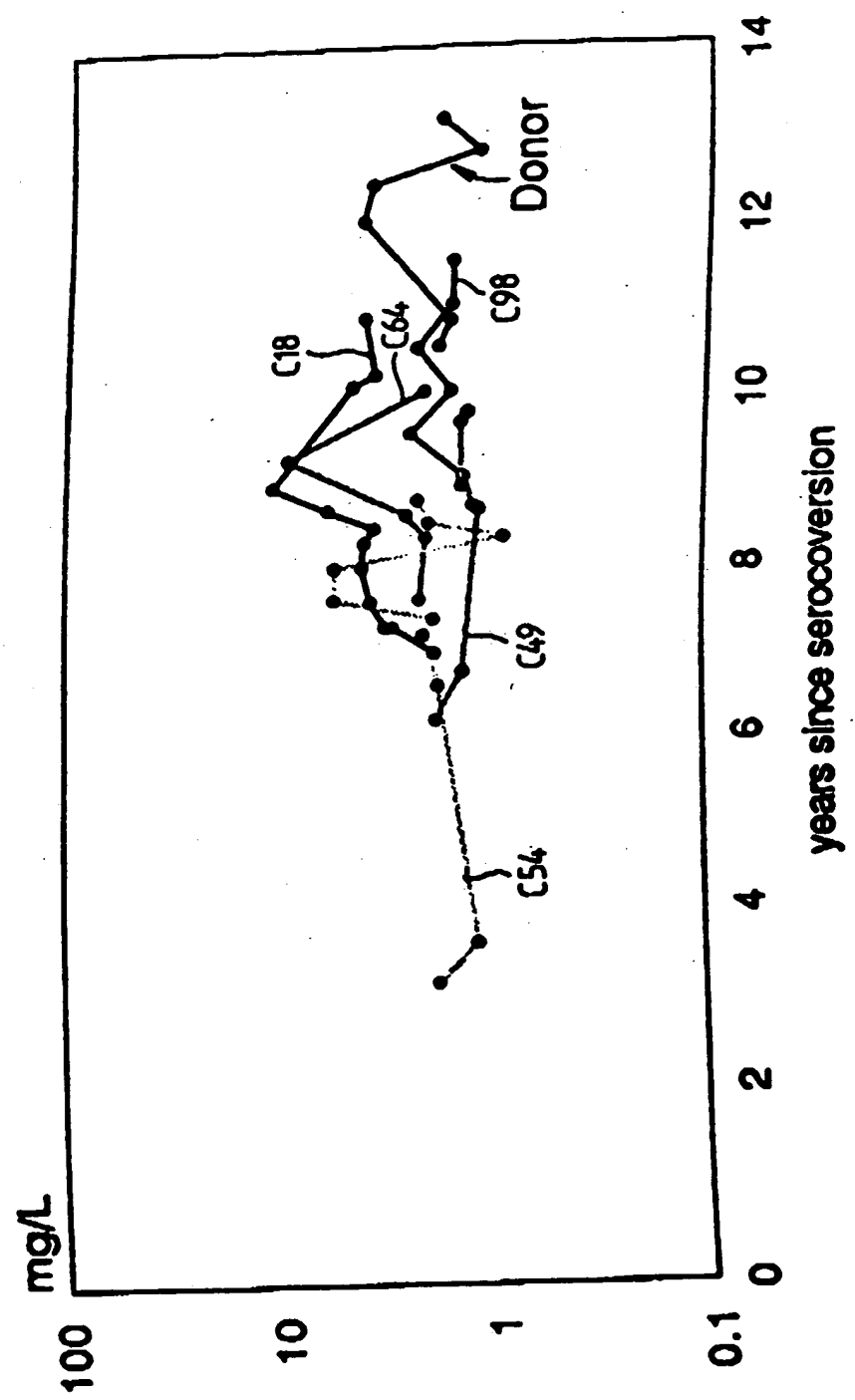


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trends in beta-2 microglobulin since seroconversion

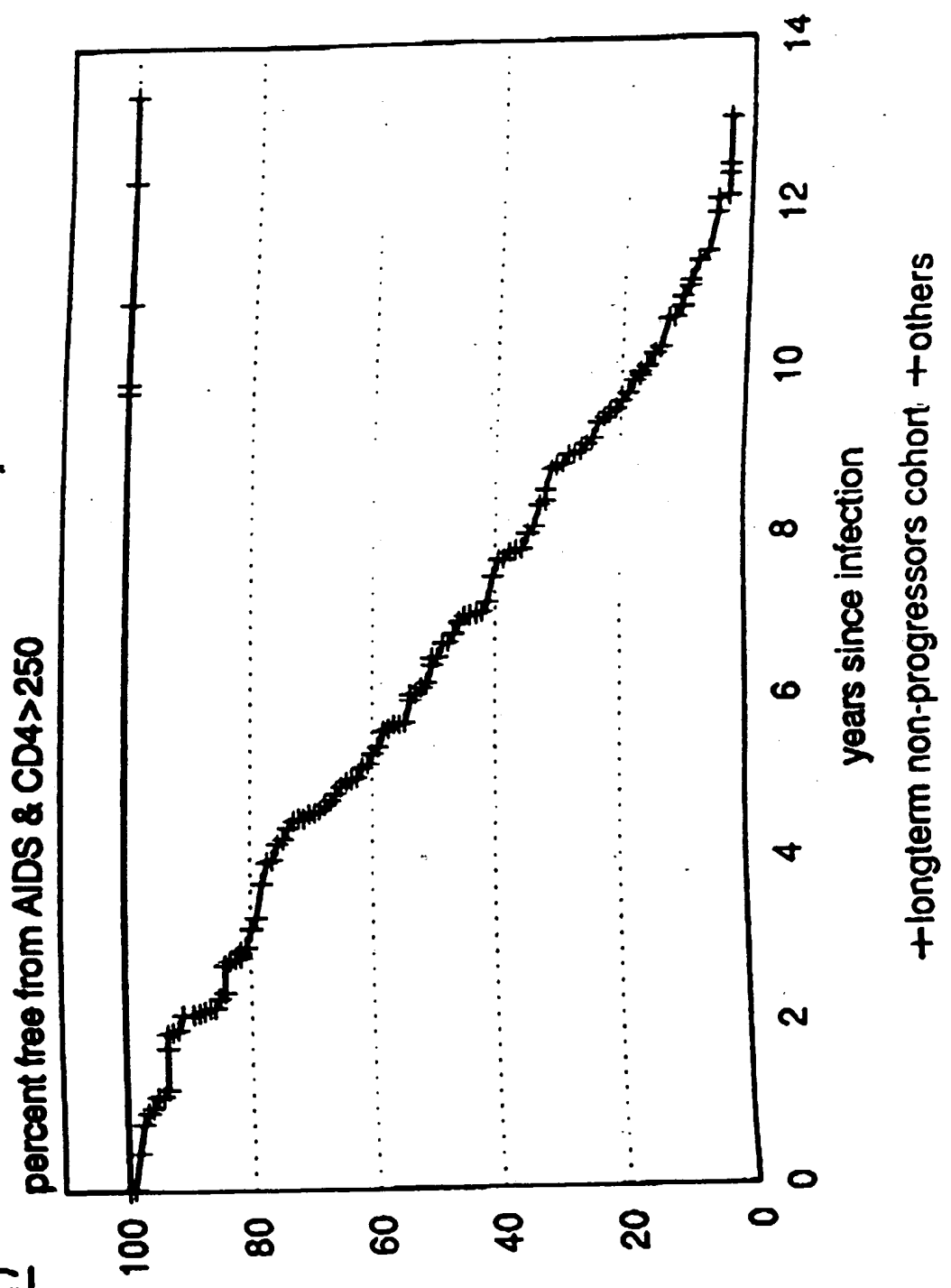
FIG 10 (f)



beta-2 microglobulin plotted on a log scale

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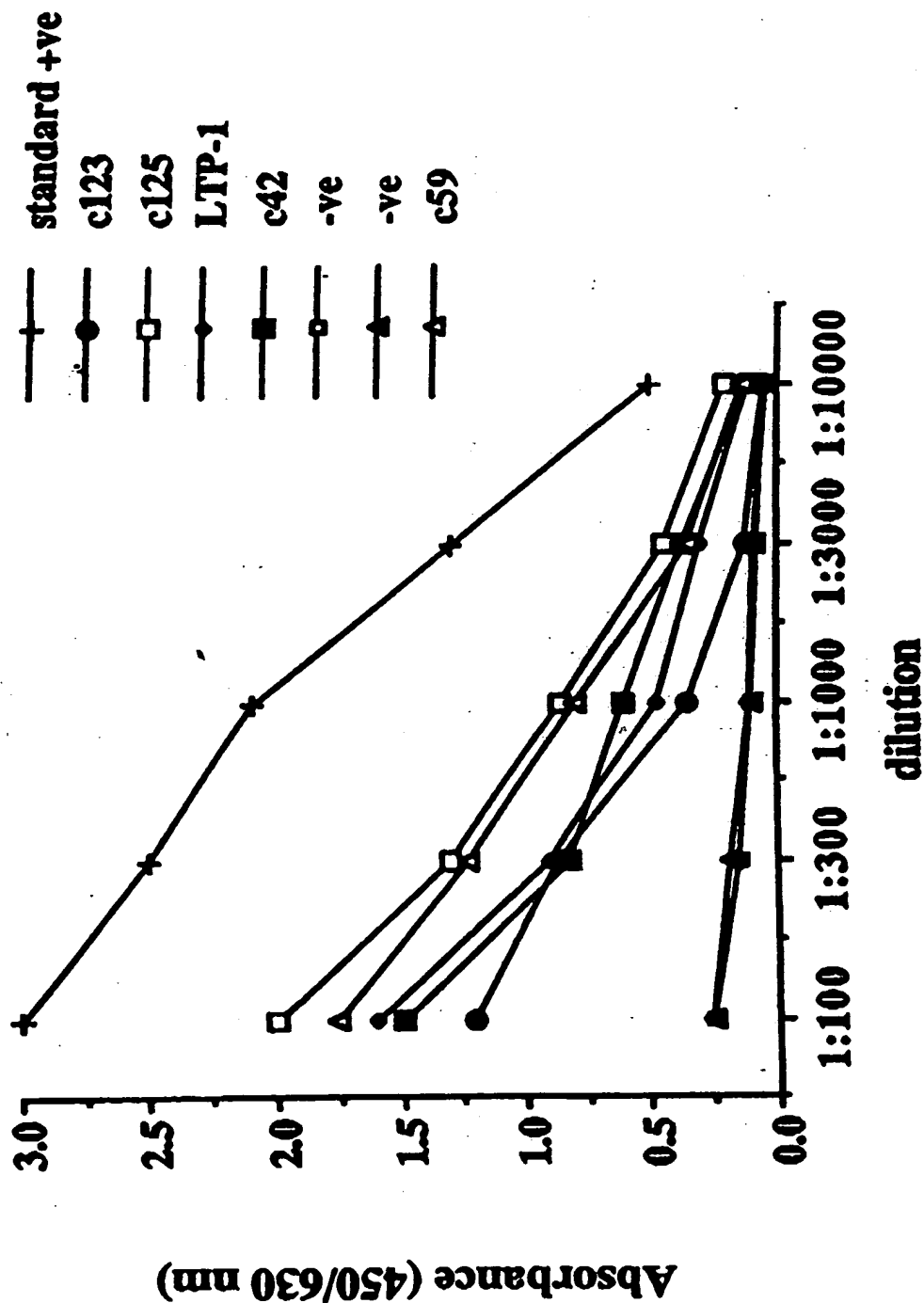
FIG 10(g)



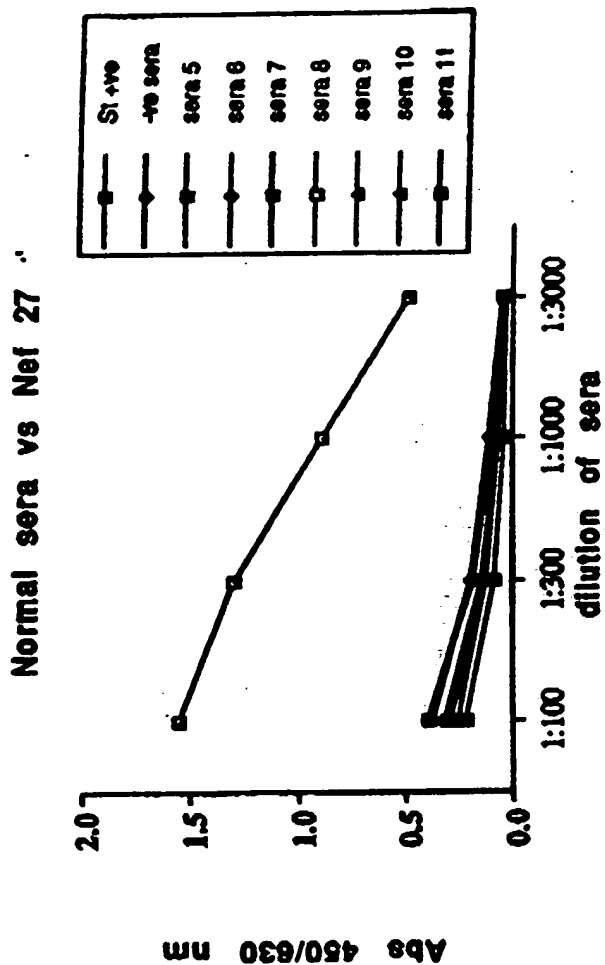


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FIGURE 12A

LTP.control gp vs Nef 27



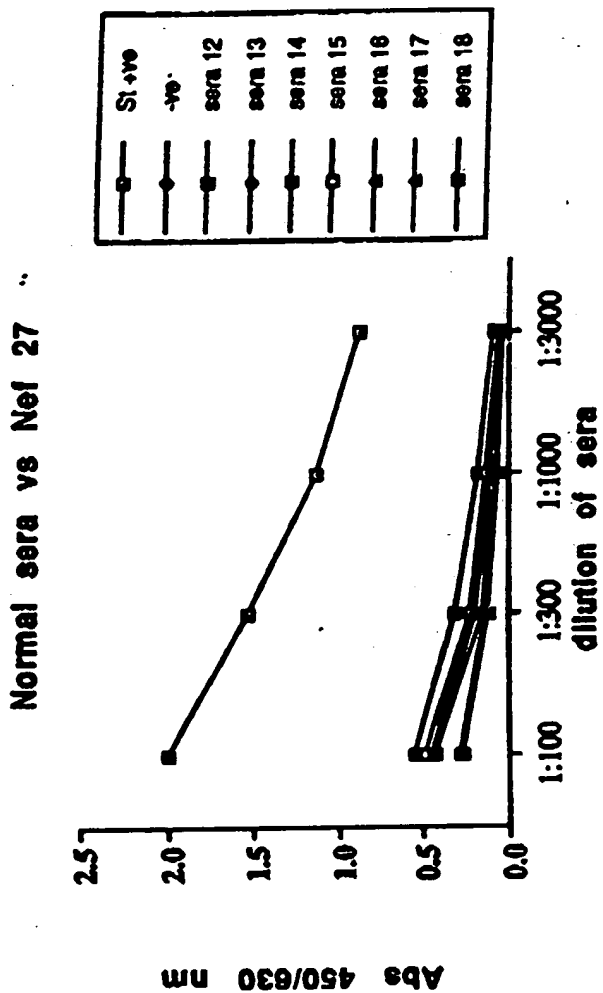
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FIGURE 12B(i)



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Normal sera 12-18

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FIGURE 12B (ii)



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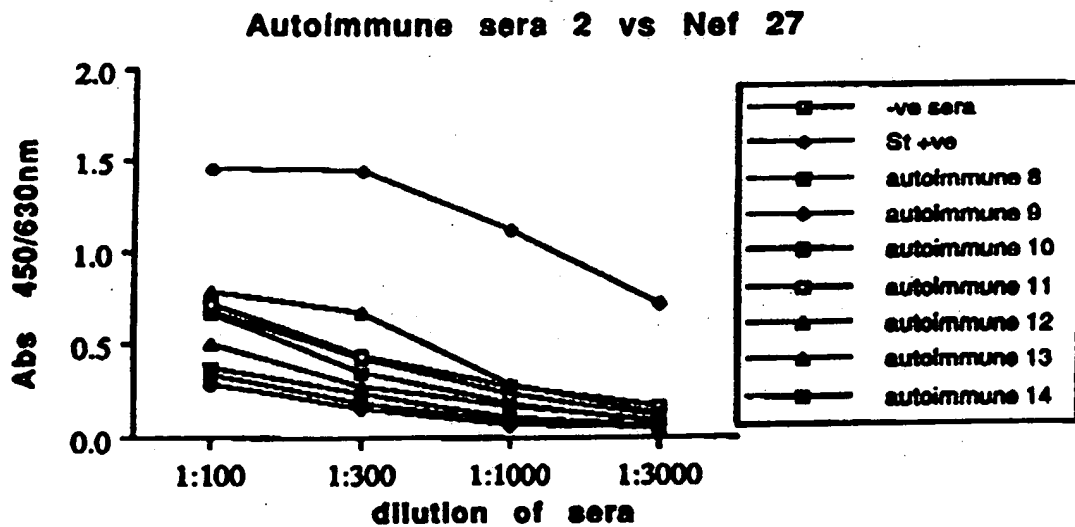
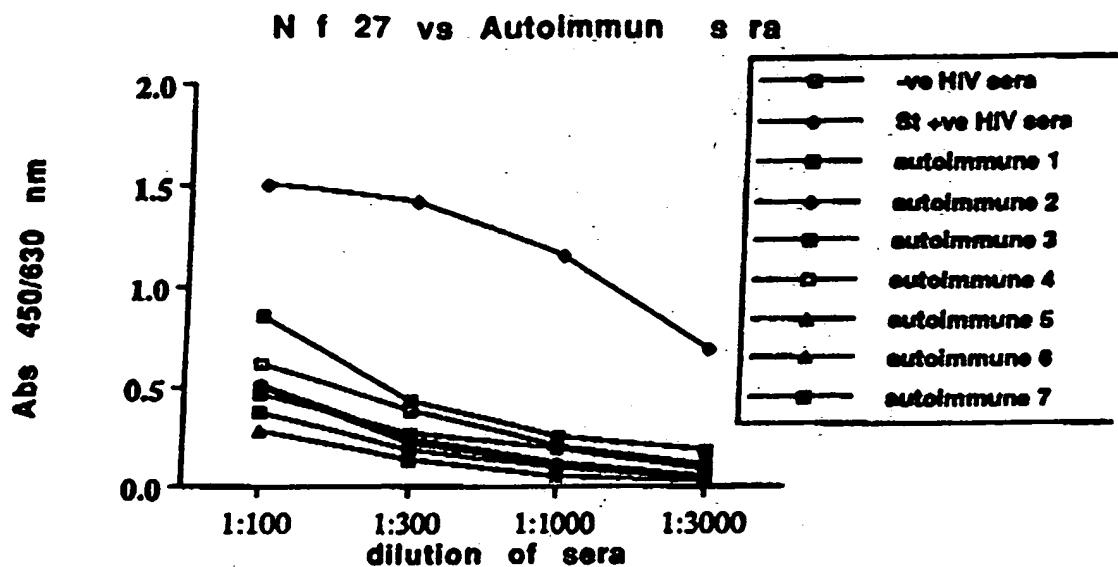


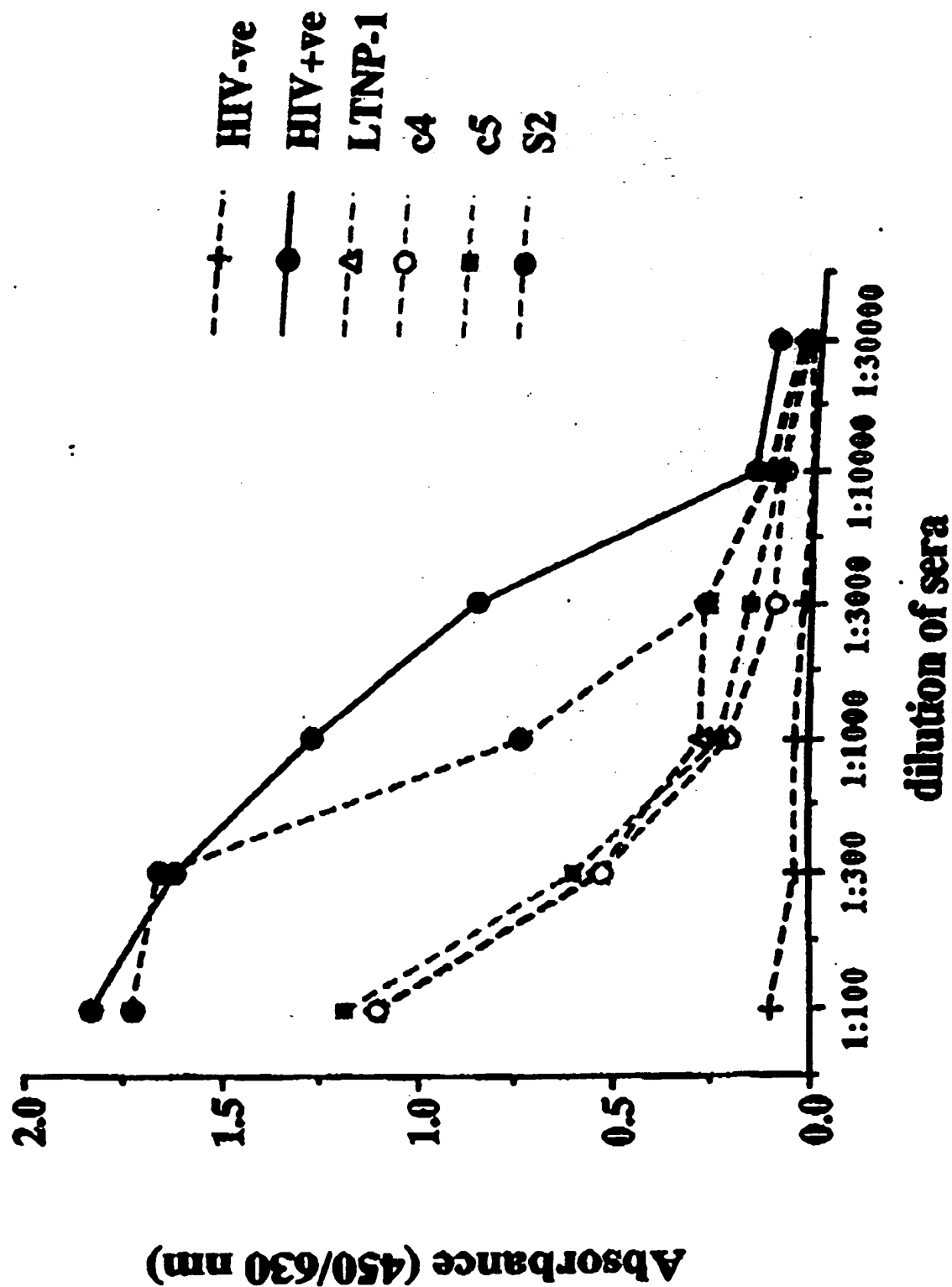
FIGURE 12B(ii)

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[illegible]

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FIGURE 12D

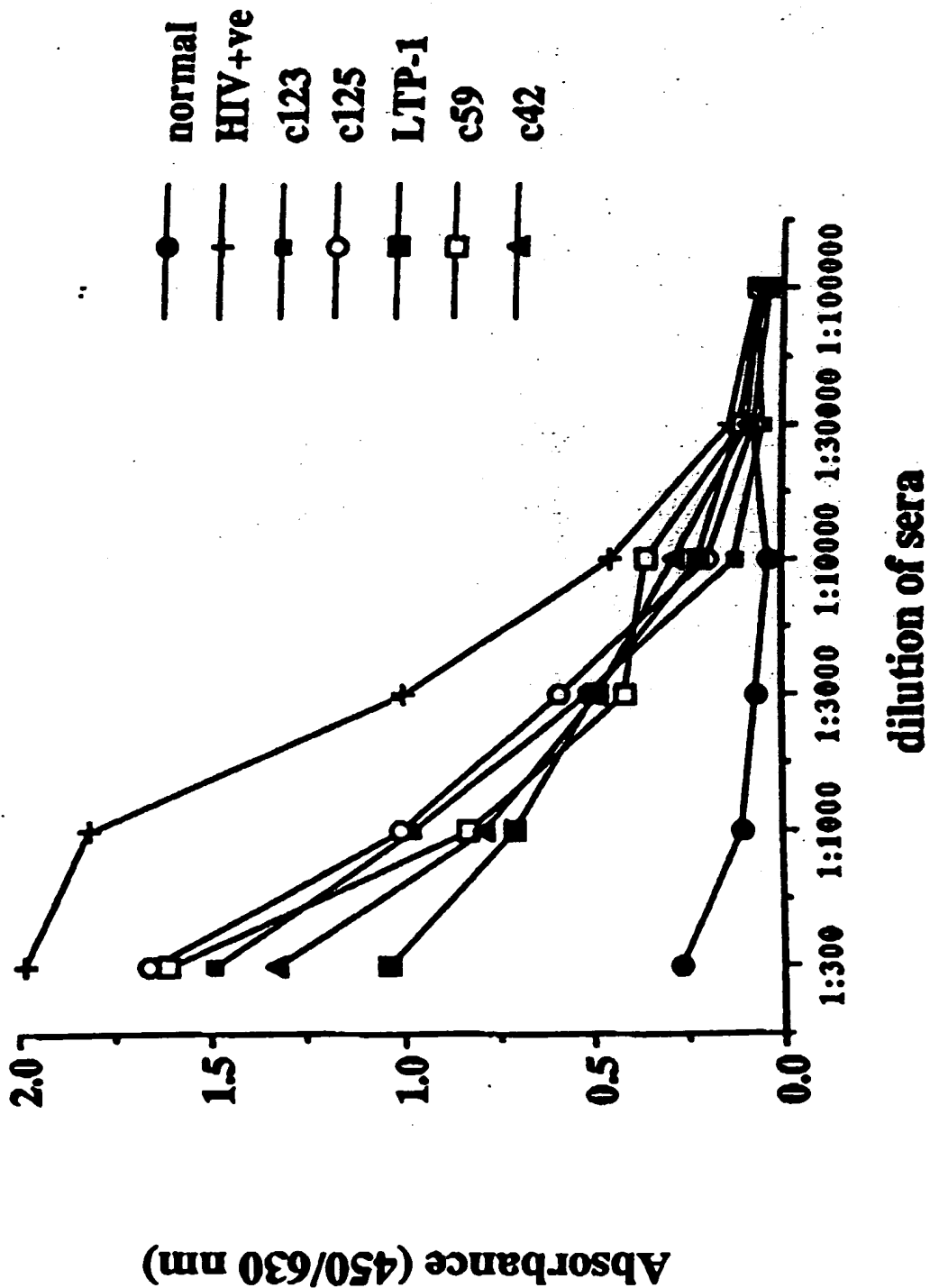
Non-progressor sera vs Nef 27



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FIGURE 13A(i)

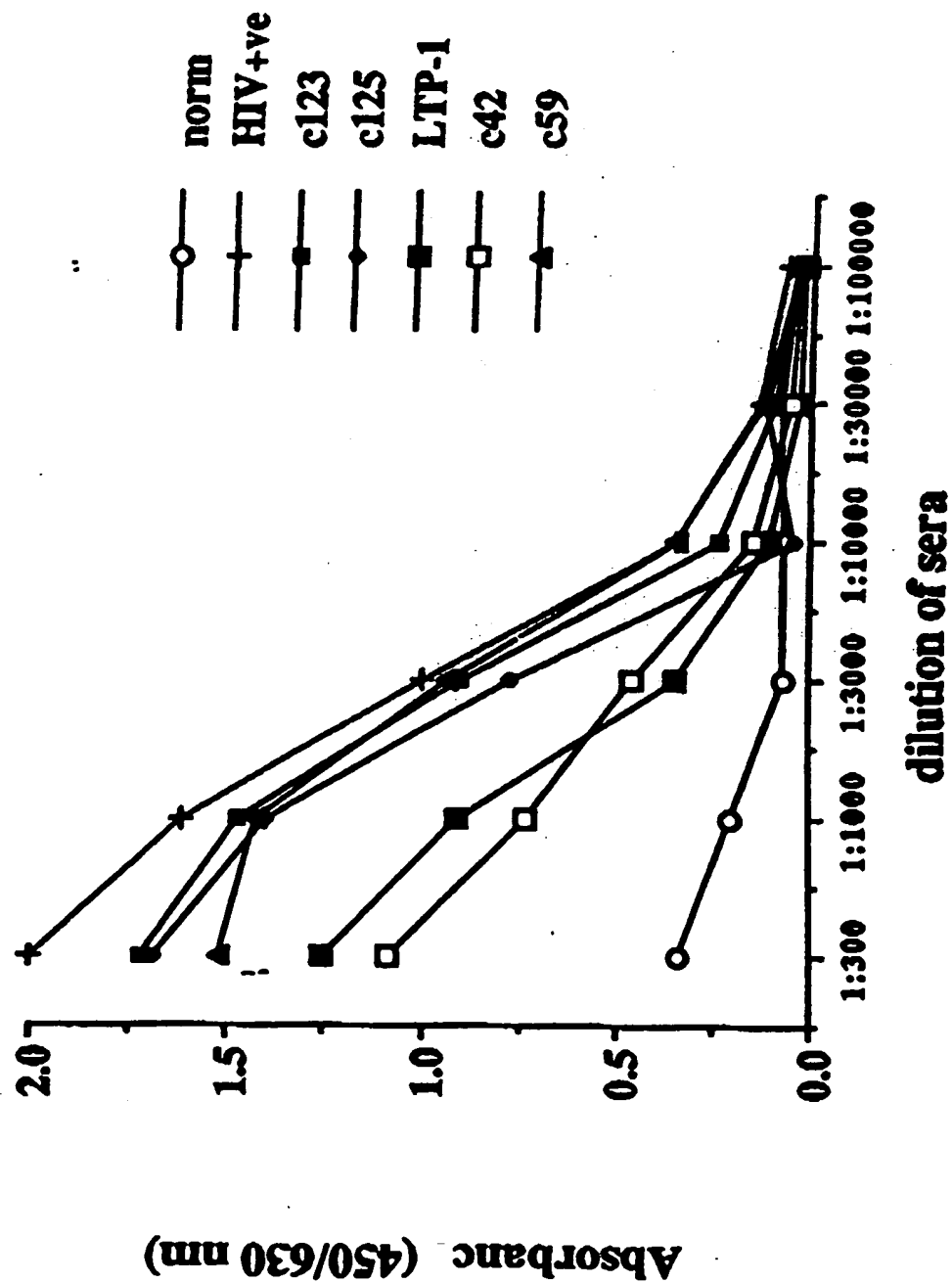
LTP gp.vs Nef aa1-19



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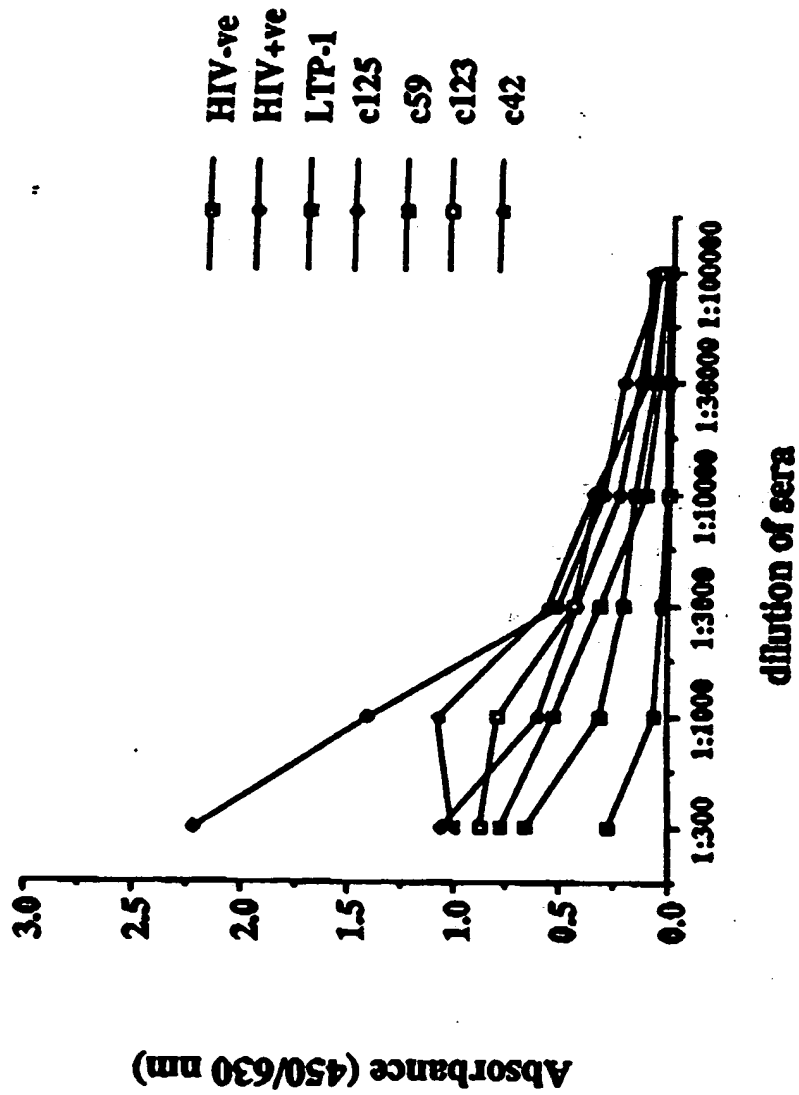
FIGURE 13A (ii)

LTP.gp vs Nef aa 20-36



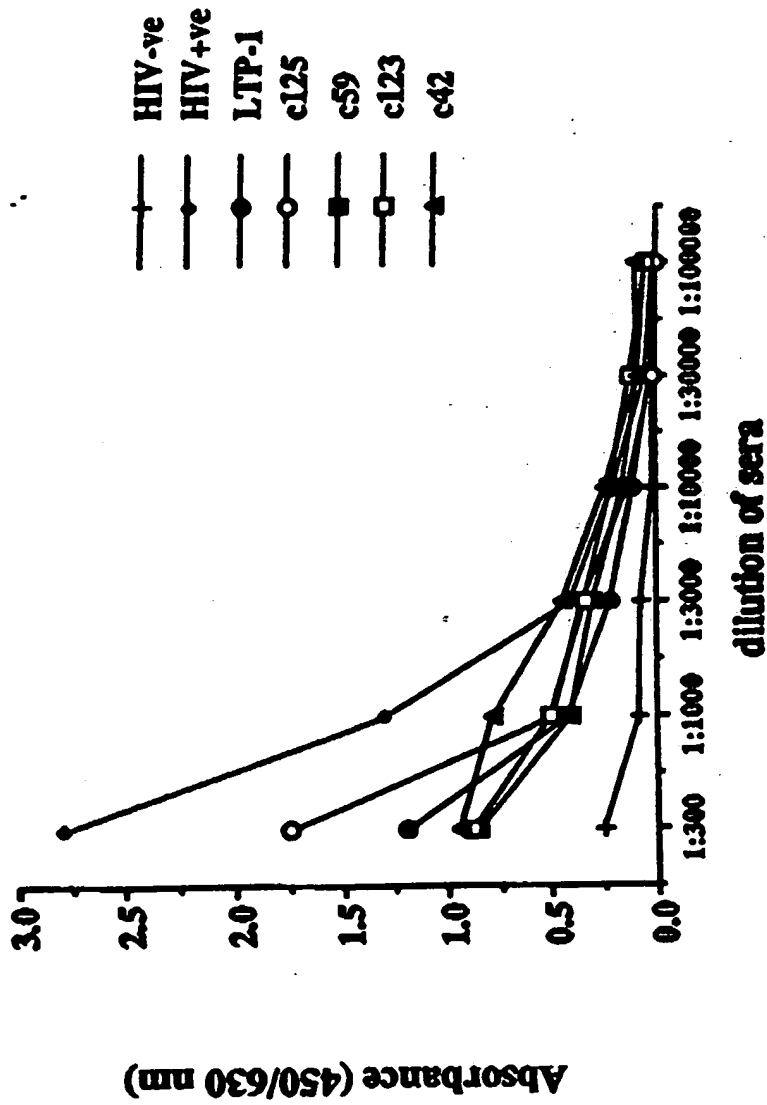
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FIGURE 13A (iii)

LTP.gp. vs Nef 44-65



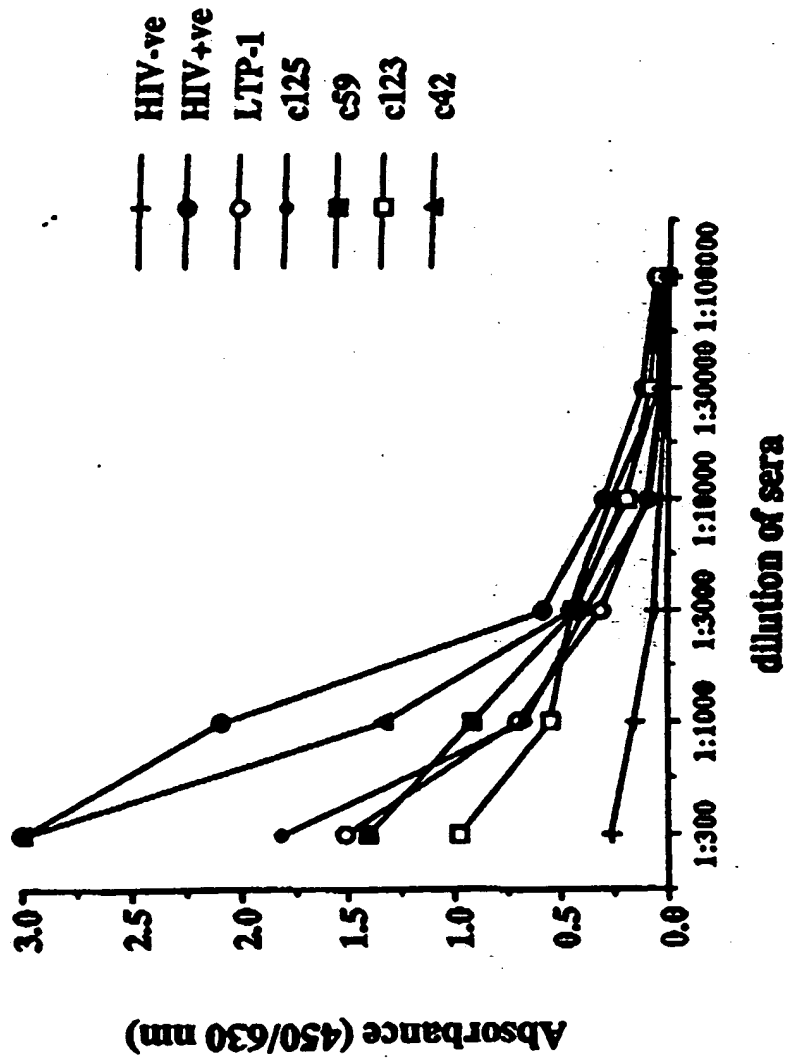
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FIGURE 13A (iv)

LTP.gp. vs Nef aa 72-83



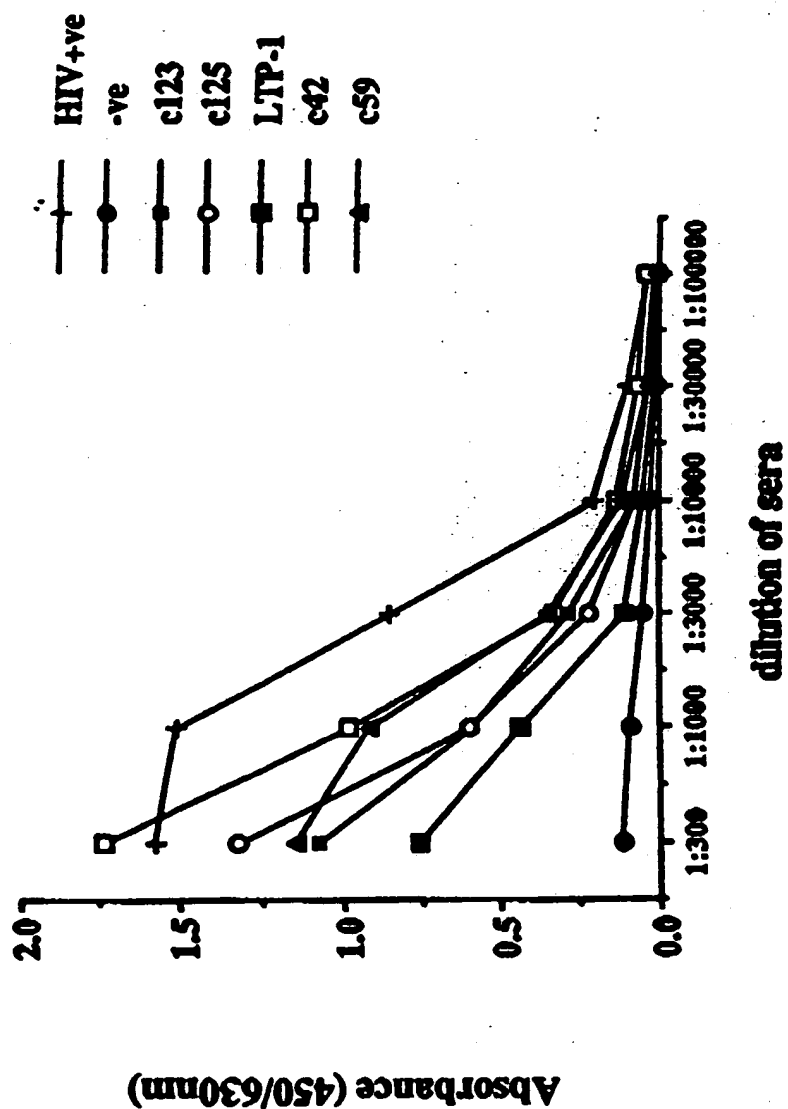
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FIGURE 13A (v)

LTP.gp. vs Nef aa 89-97



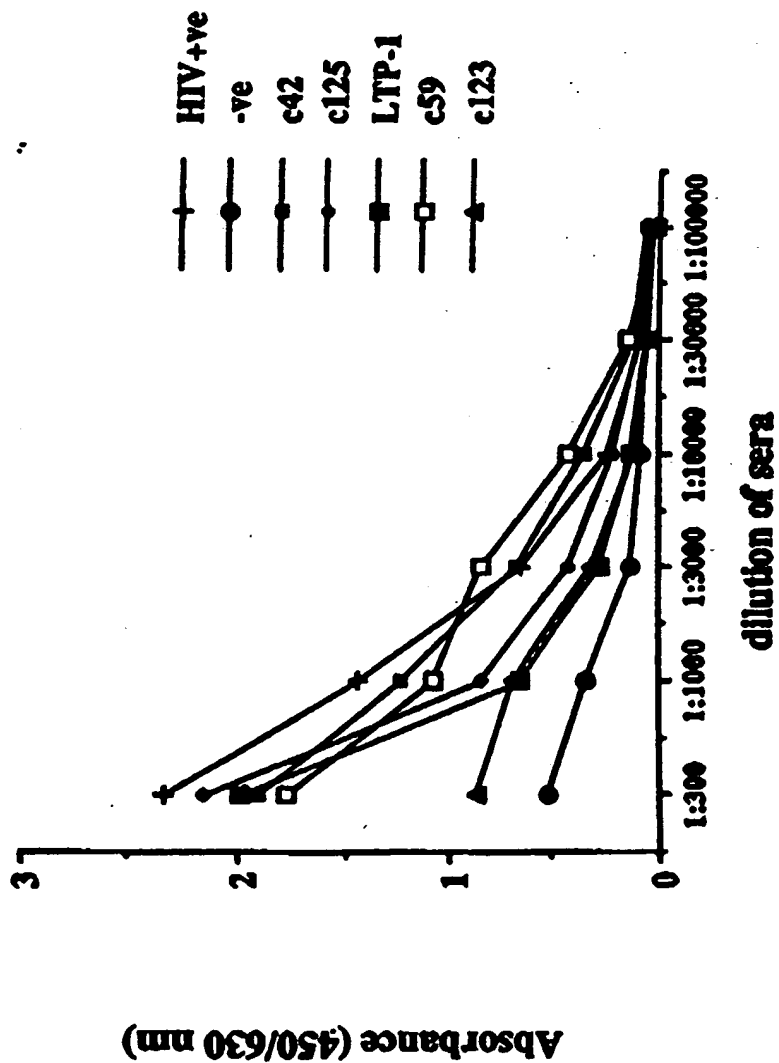
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FIGURE 13A (vi)

LTP.gp vs Nef aa 109-114



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FIGURE 13A (ii)

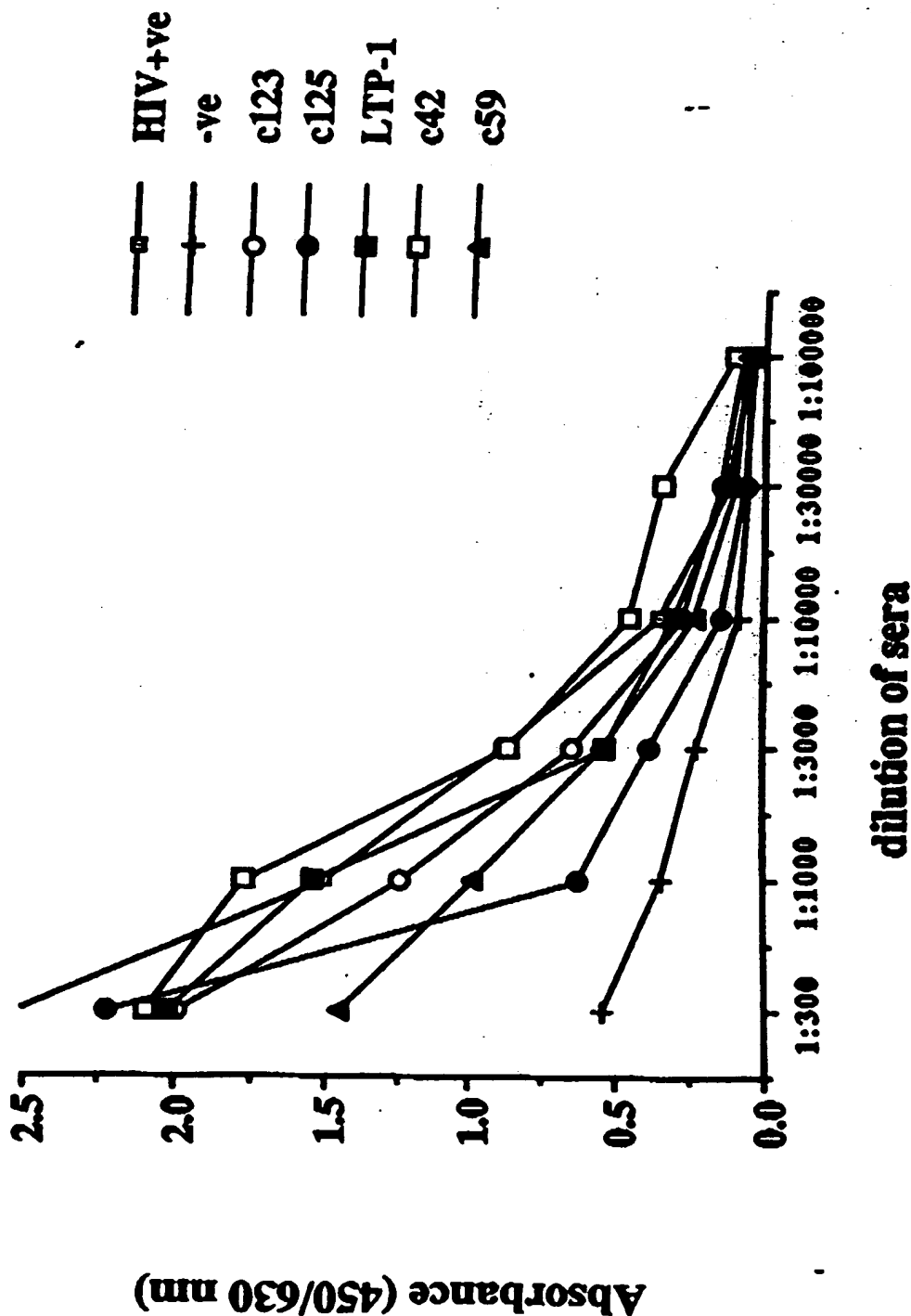
LTP gp.vs Nef aa 121-135



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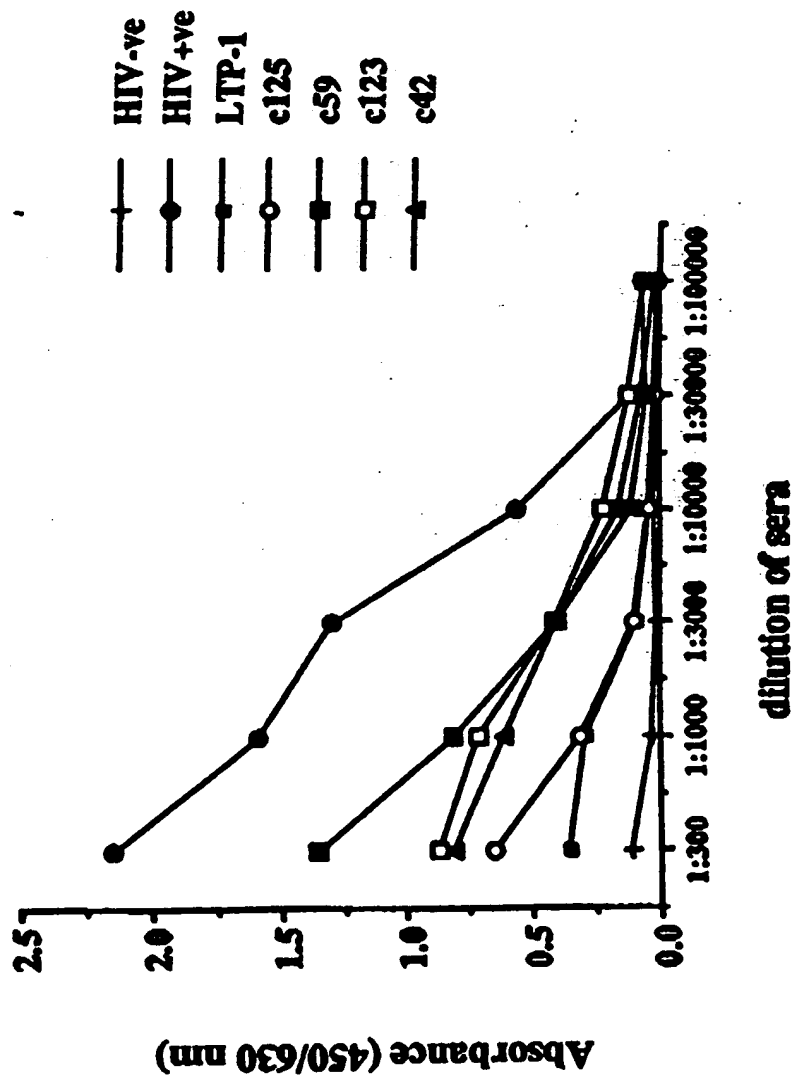
FIGURE 13A (vii)

LTP.gp vs Nef 162-177

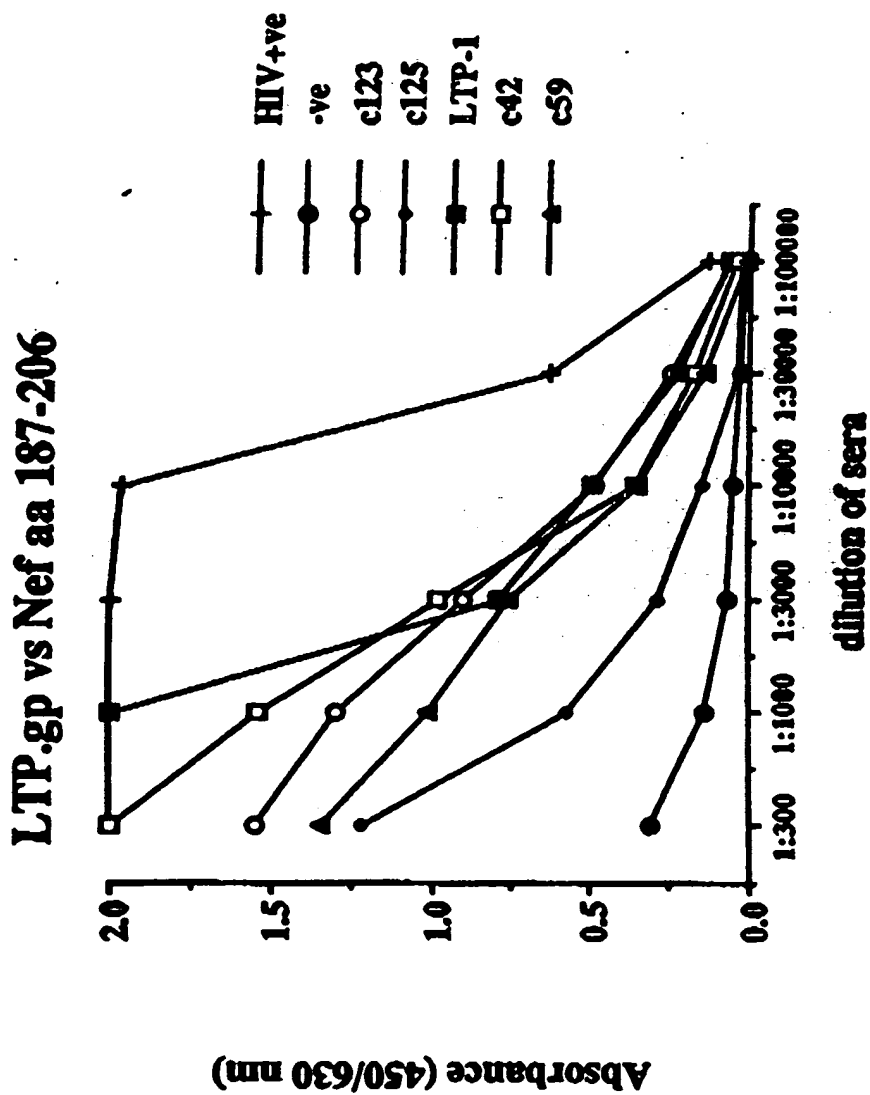


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FIGURE 13A (ik)

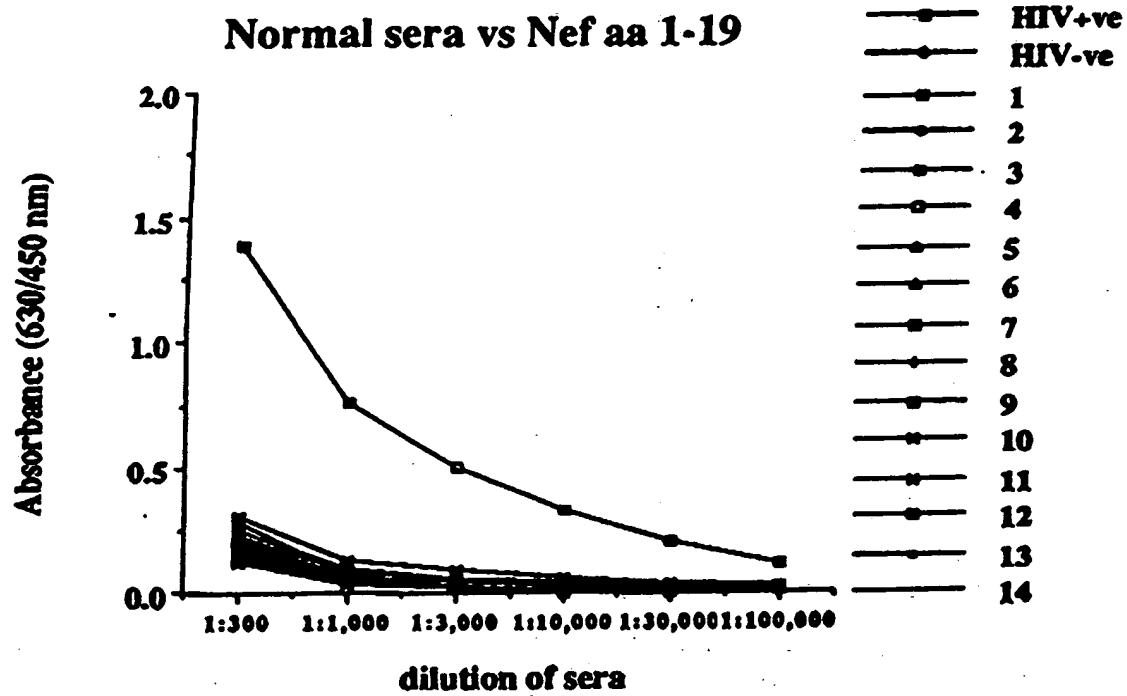
LTP.gp. vs Nef 164-186



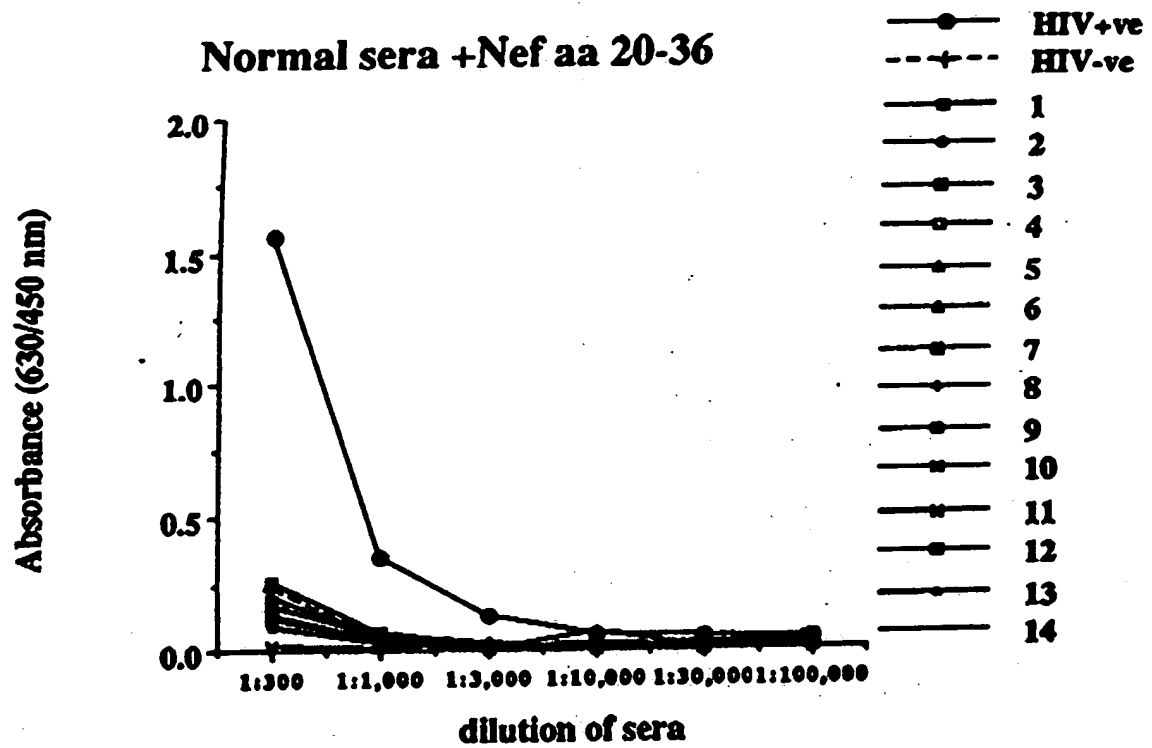
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FIGURE 13A(x)



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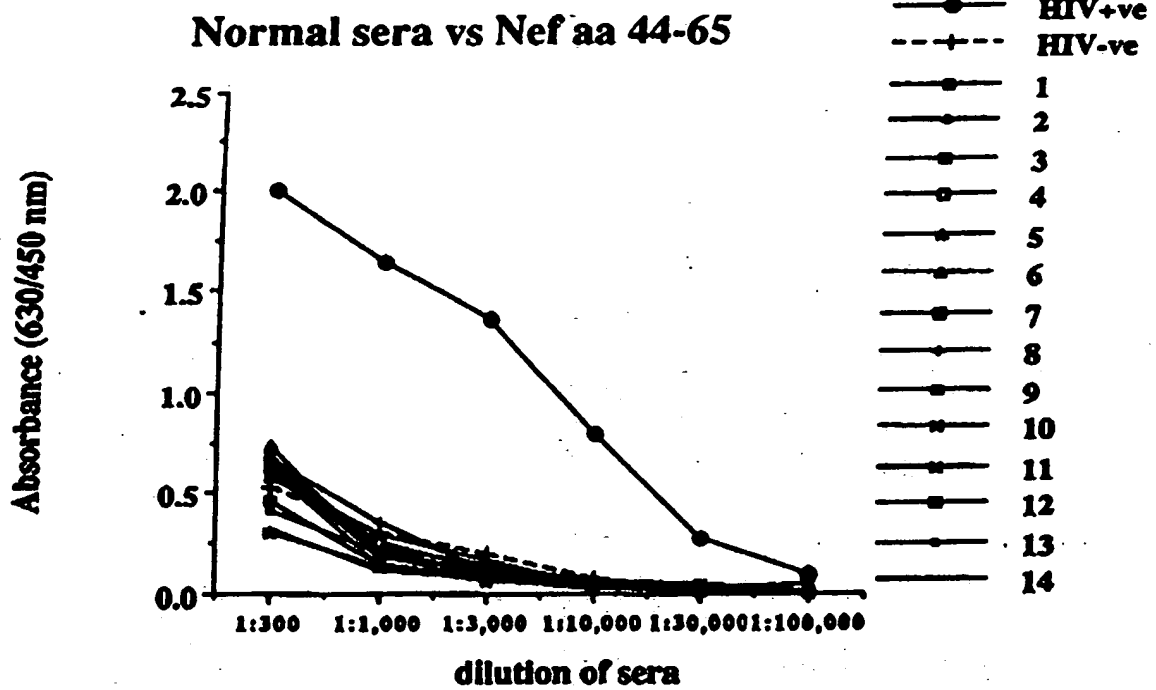


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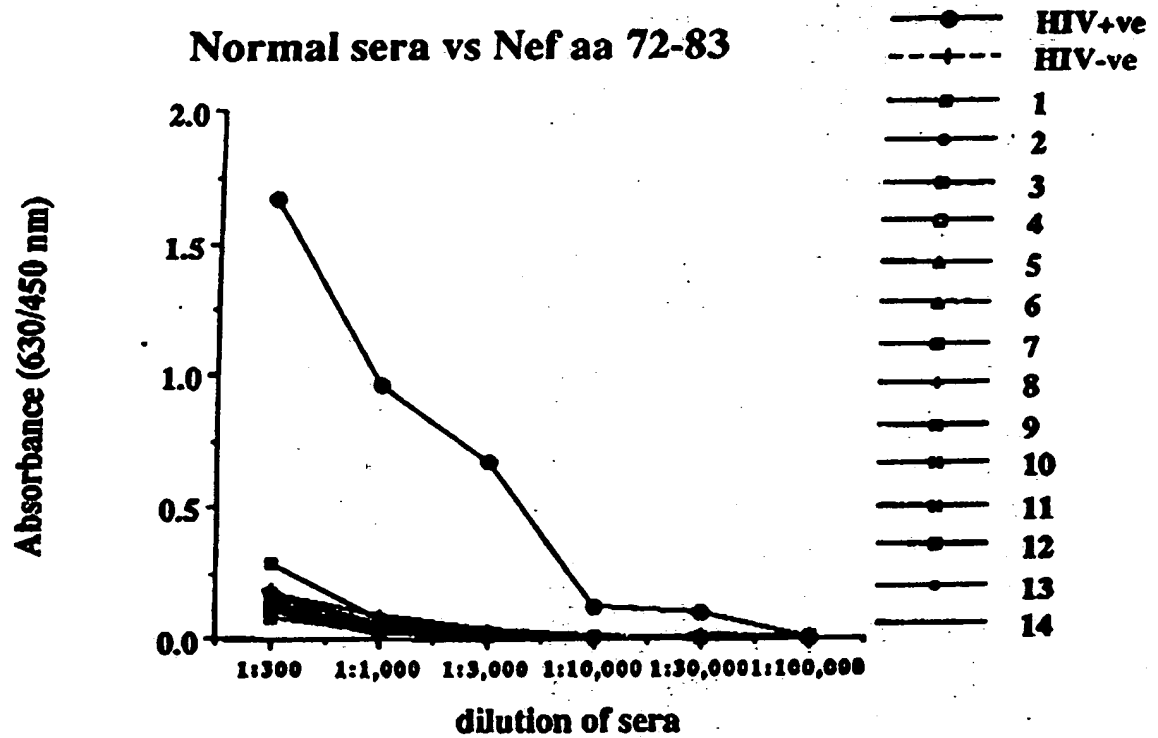
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FIGURE 13B (i) (ii)

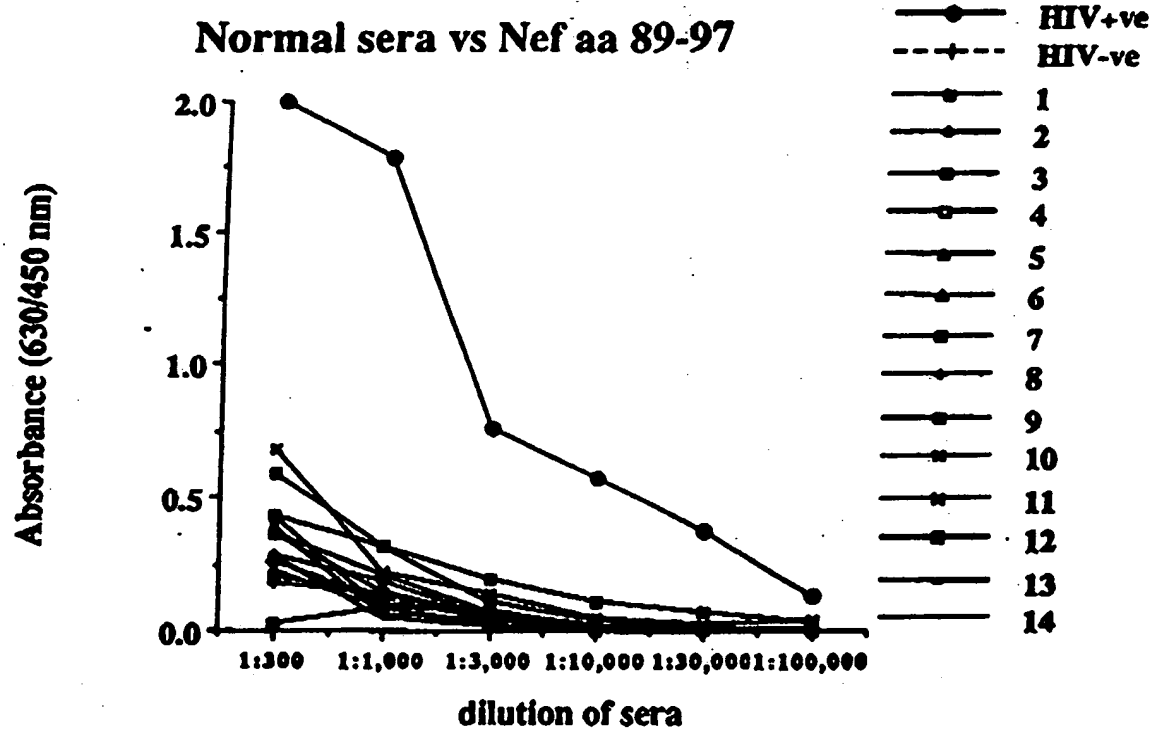


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FIGURE 13B (i) (iv)



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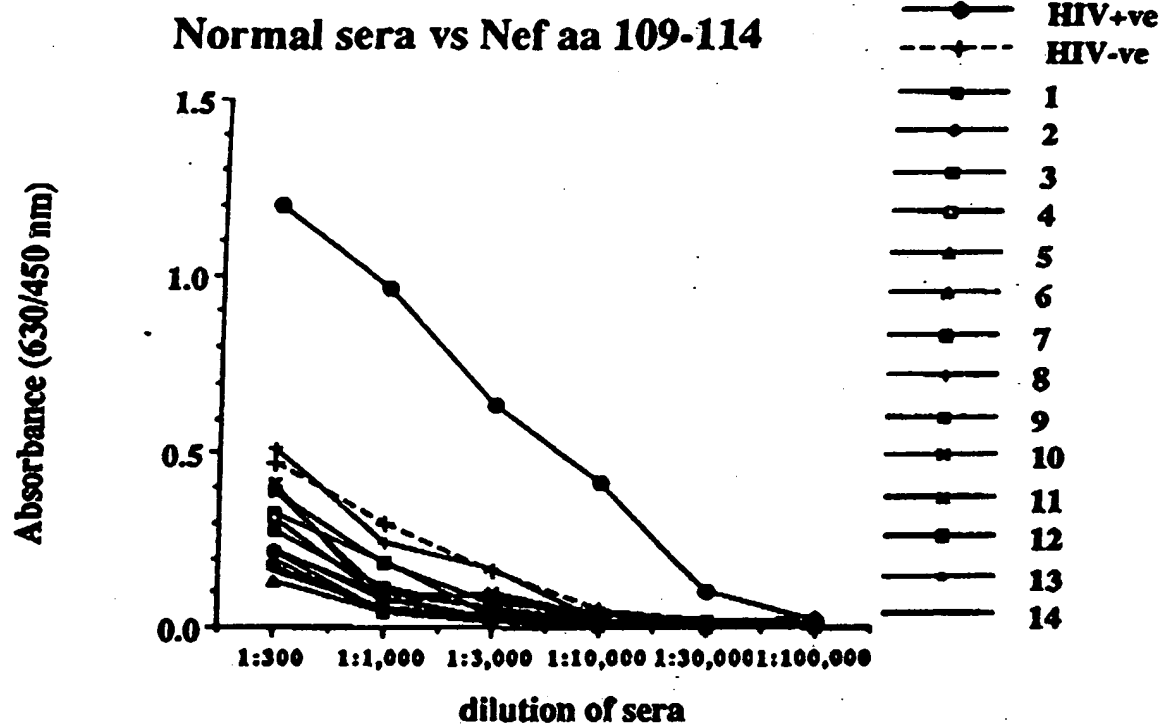


FIGURE 13 B (i) (vii)

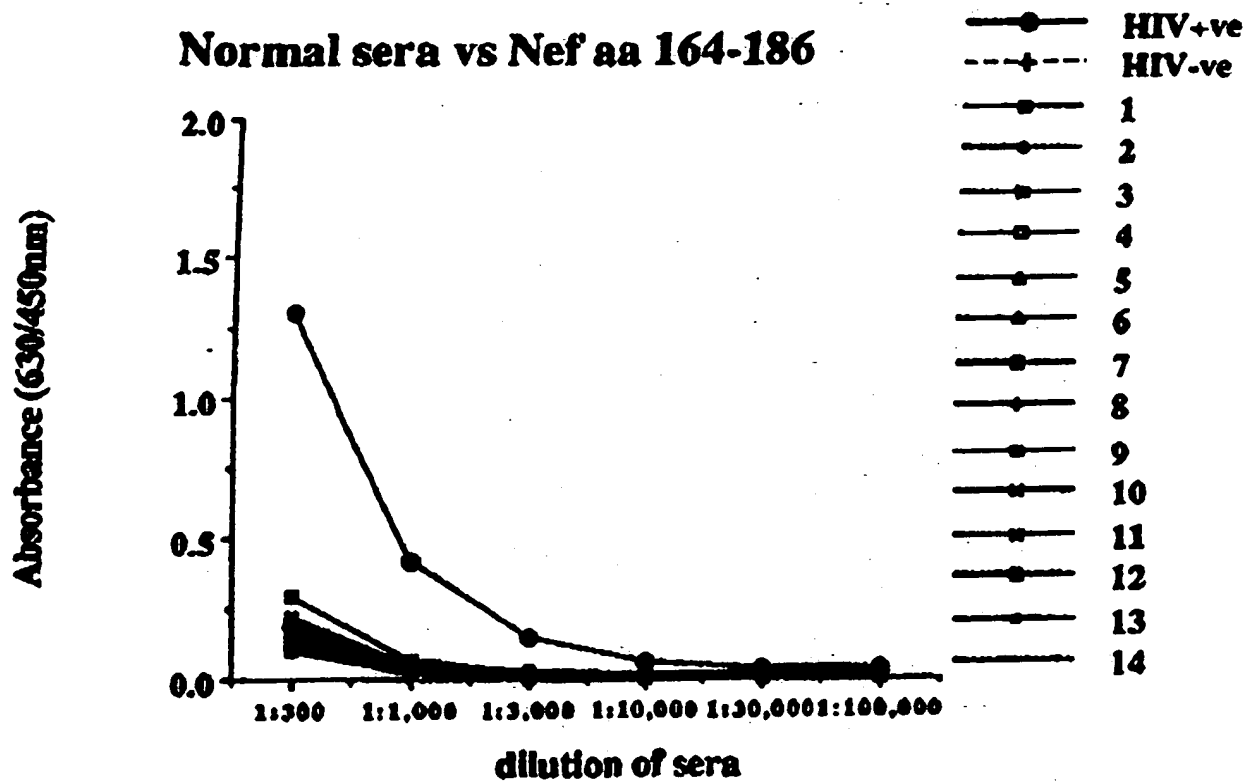




FIGURE 13B (i) (ix) ^{70/101}

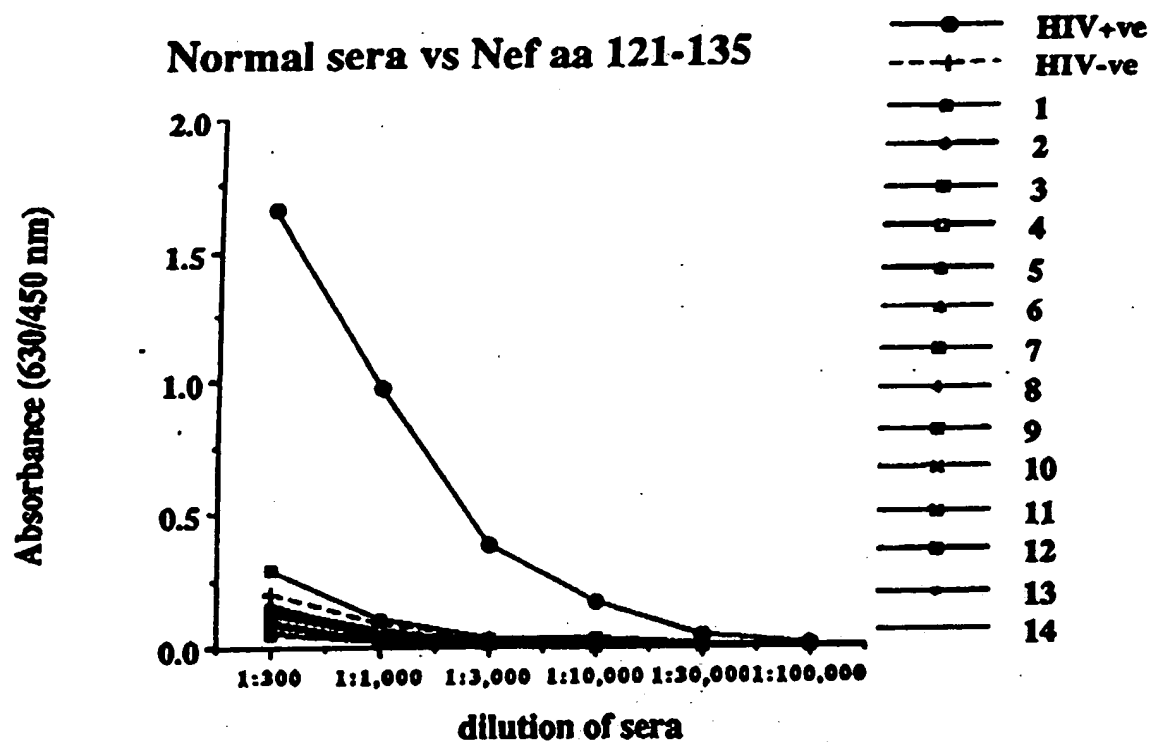
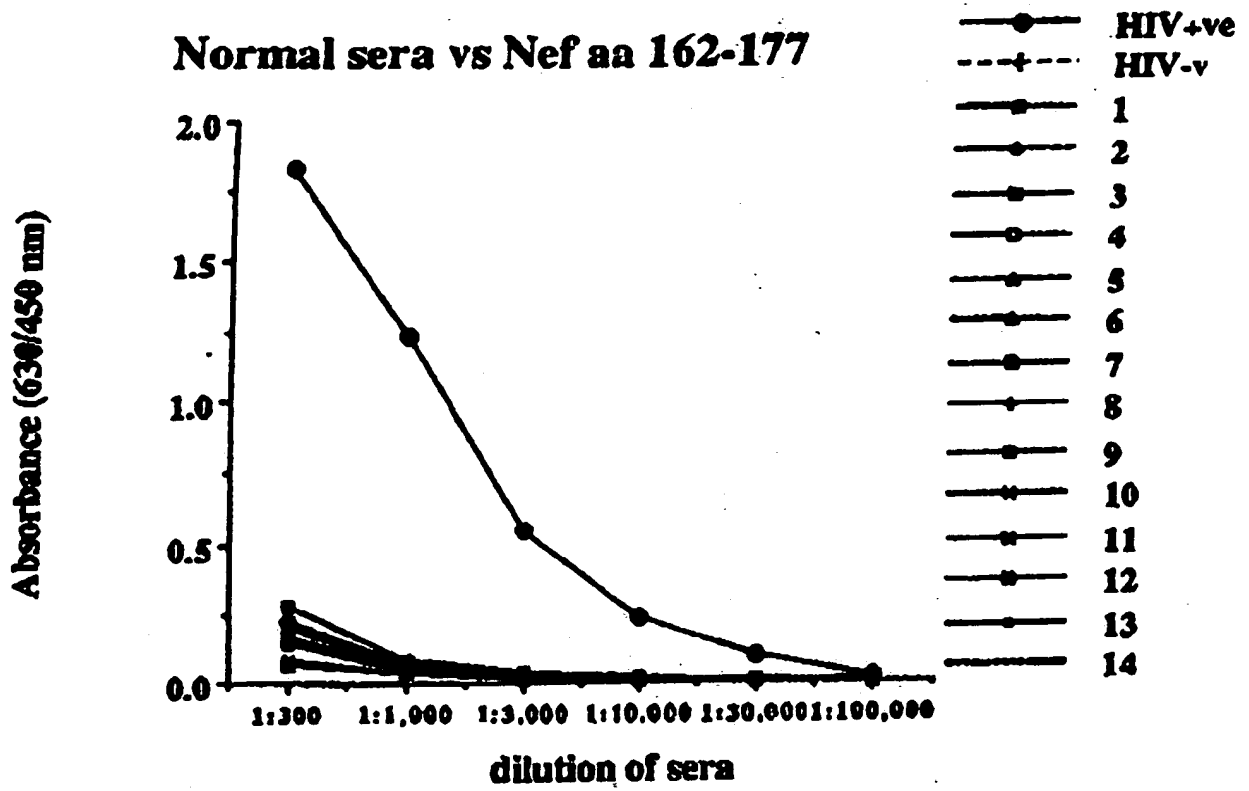


FIGURE 13B (i) (x)



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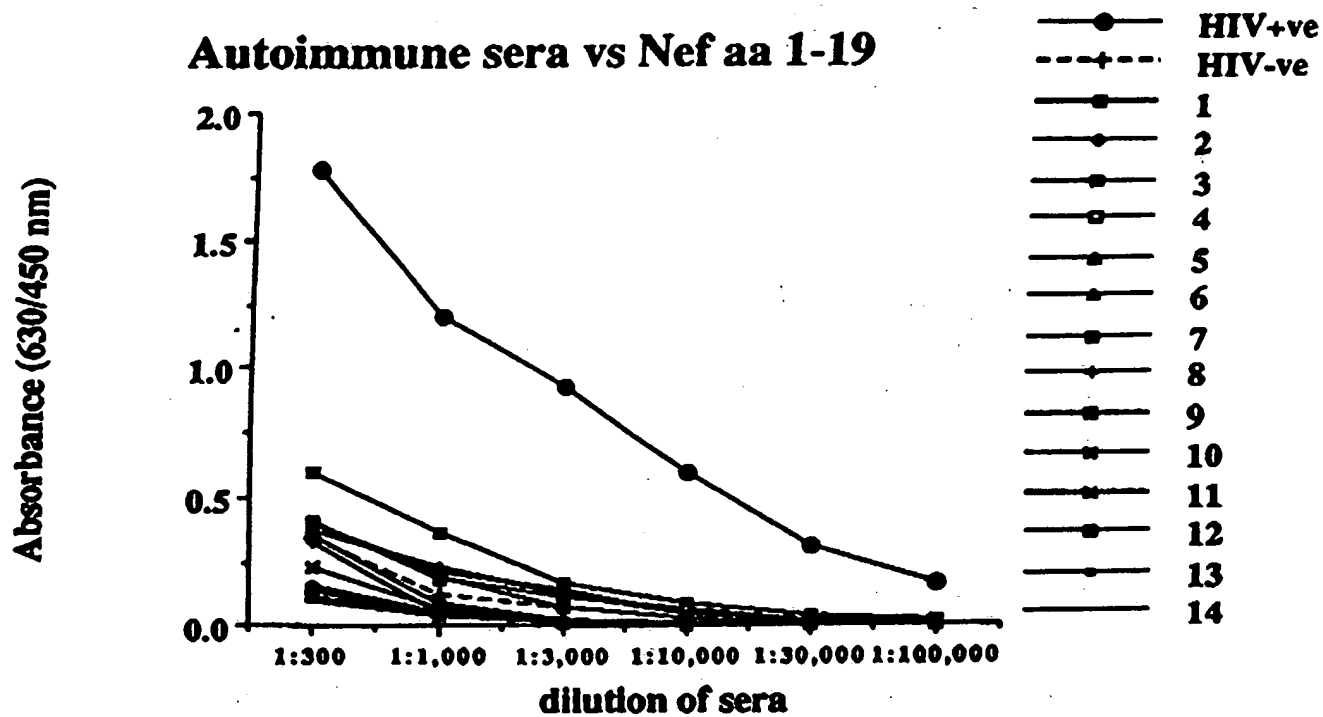
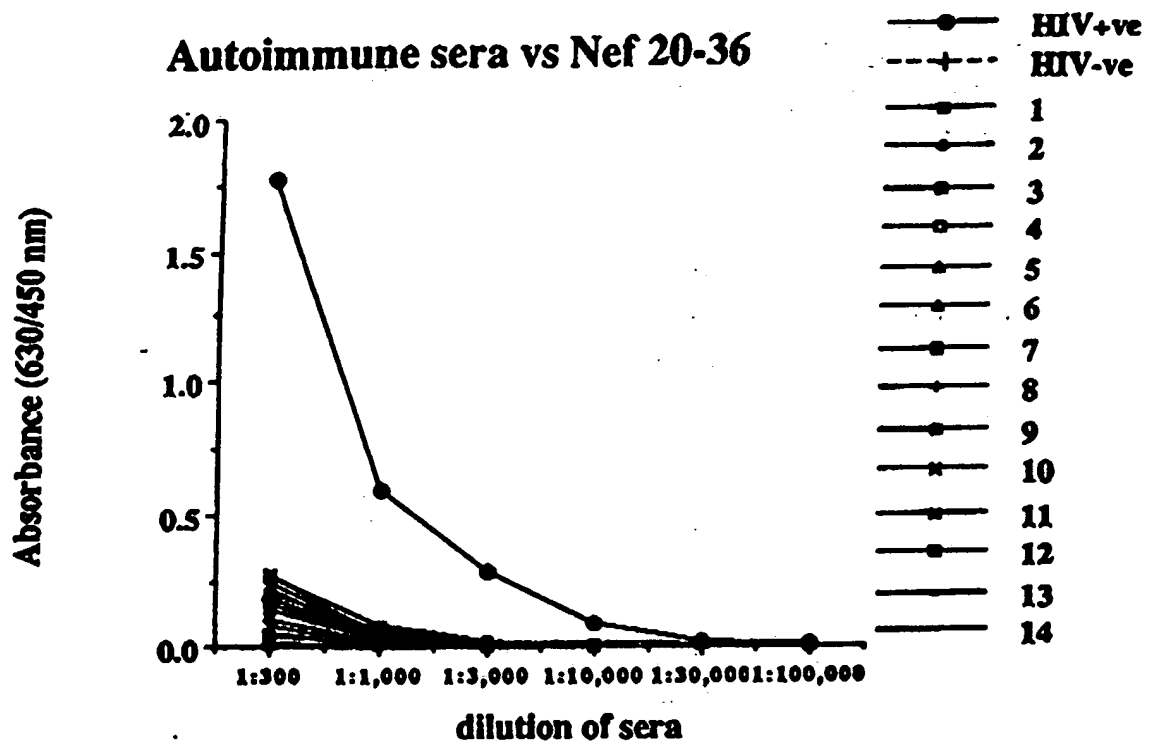
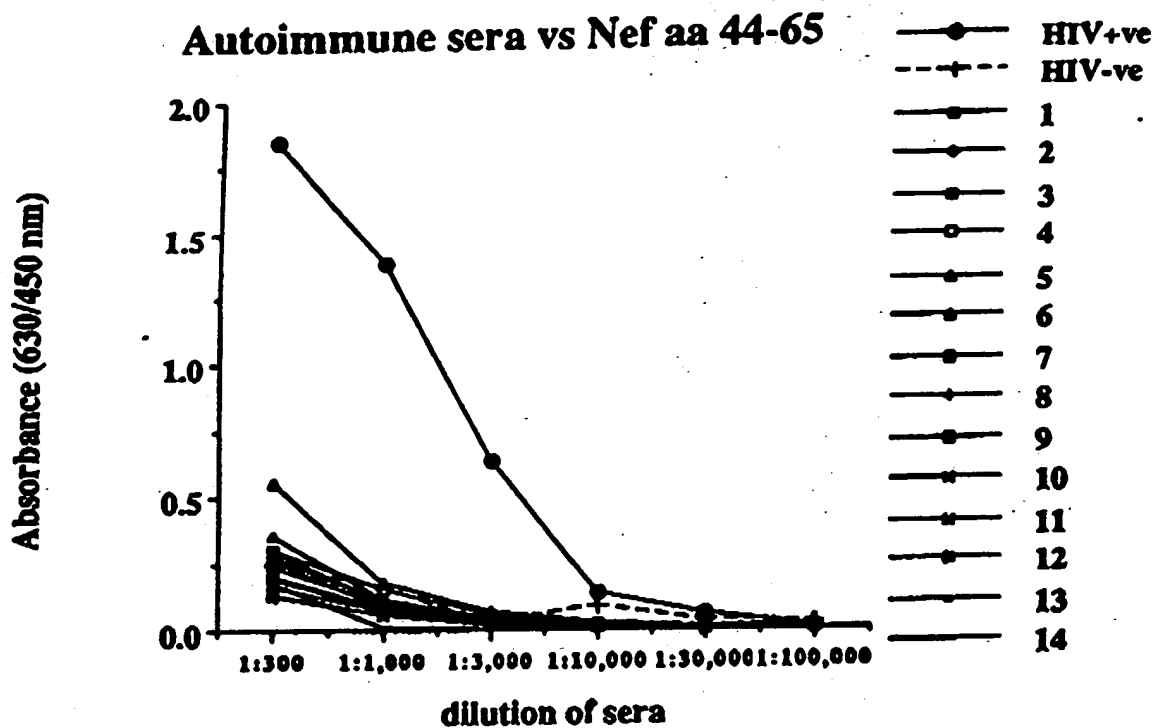


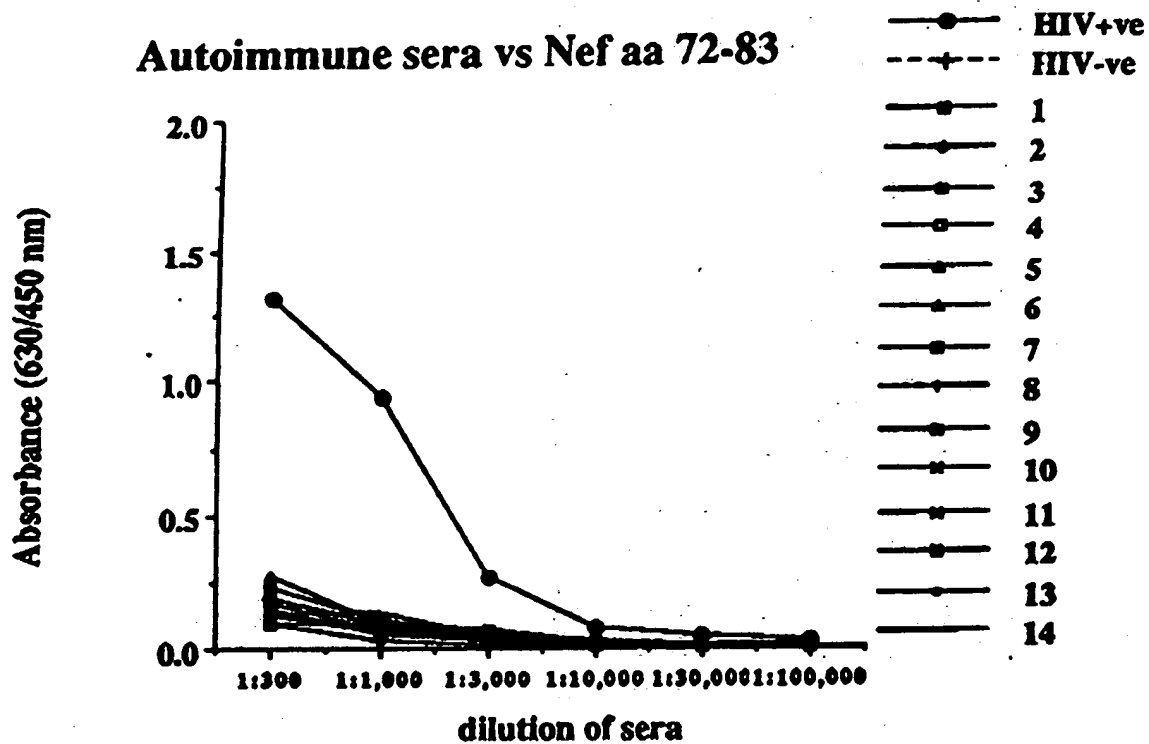
FIGURE 13 B (ii) (i) ^{73/101}



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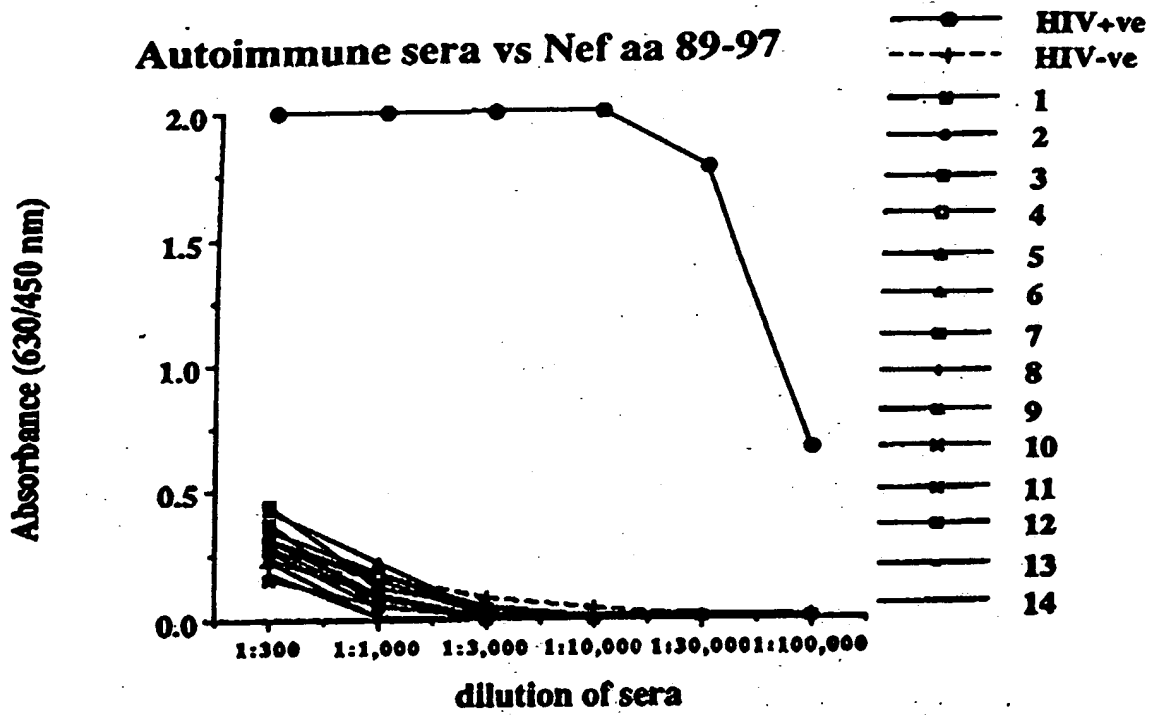


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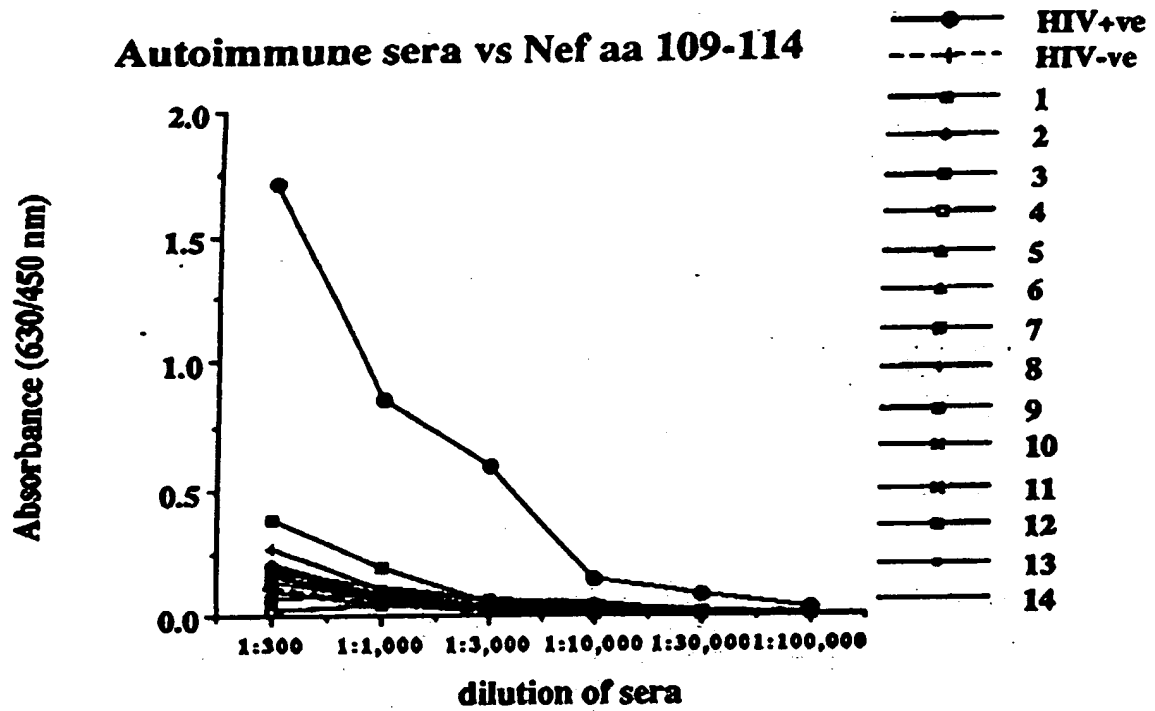


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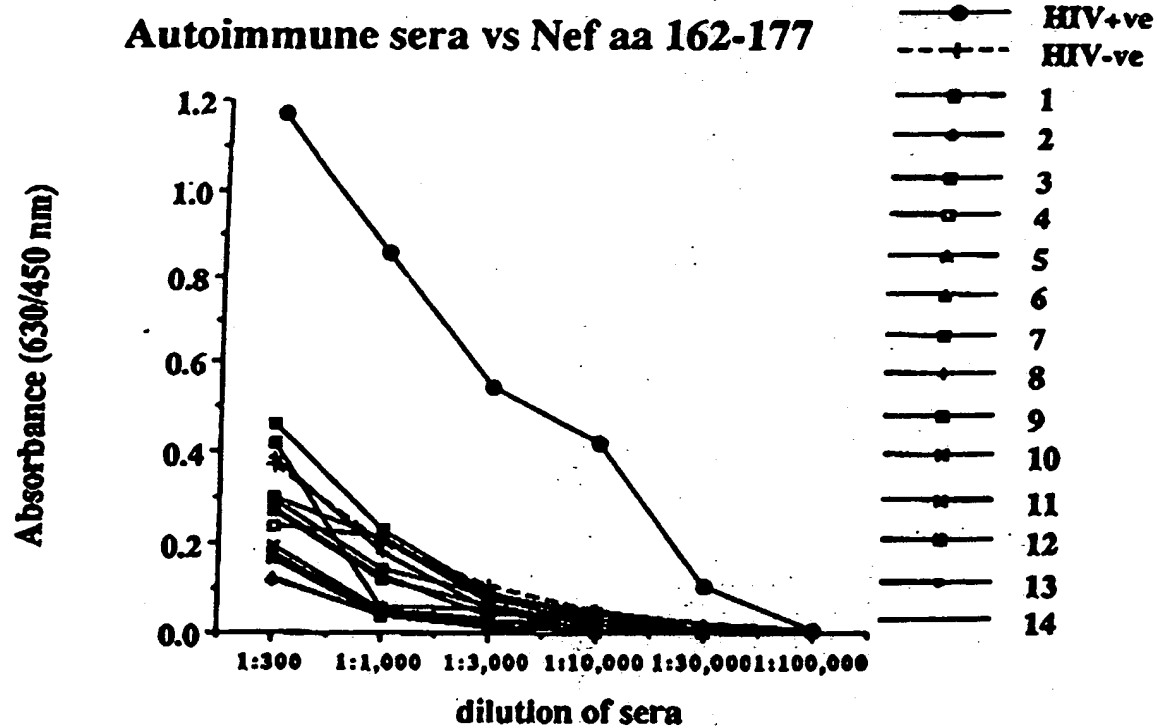
FIGURE 13(ii) (v)



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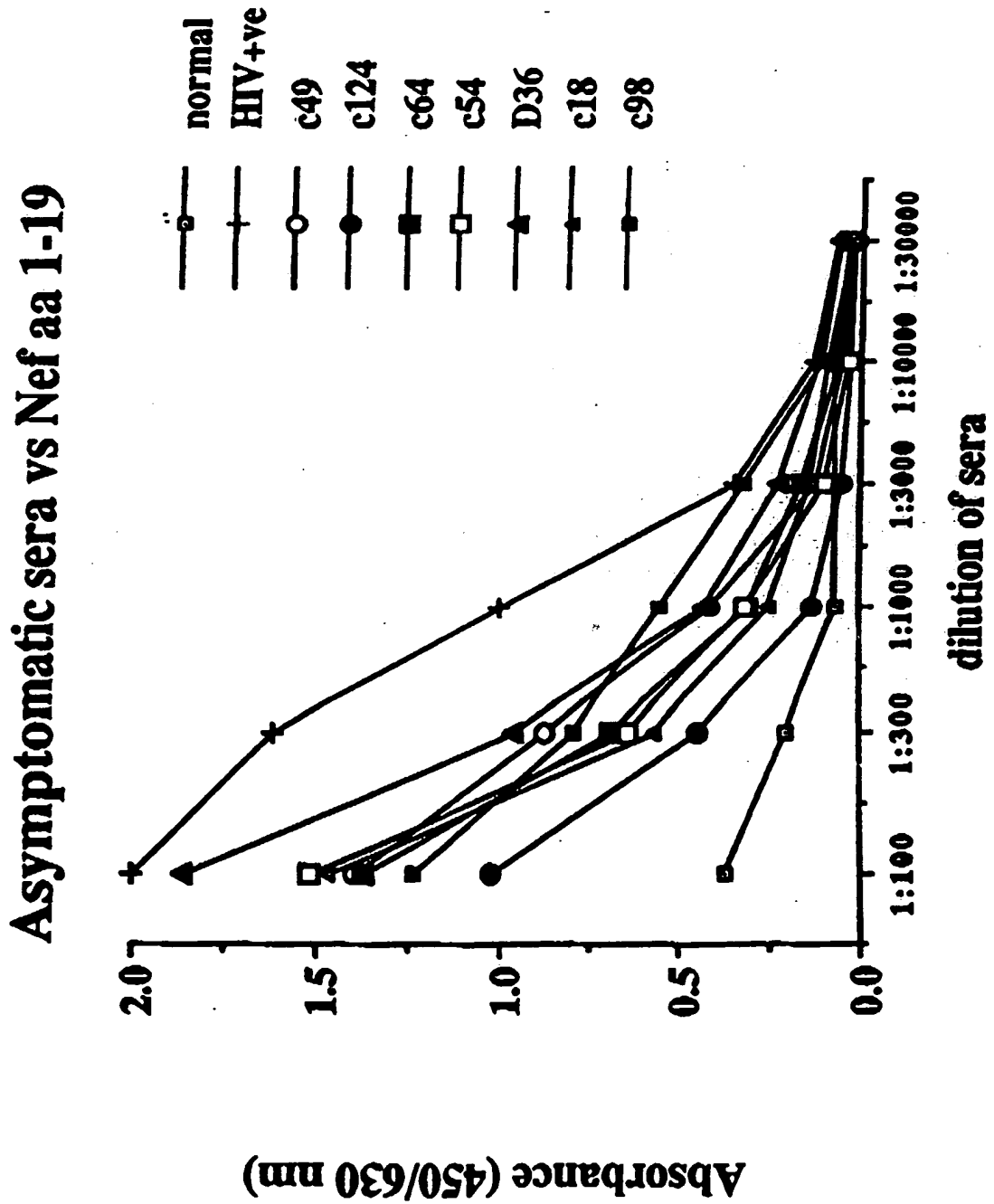


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FIGURE 13 B (11) (x)

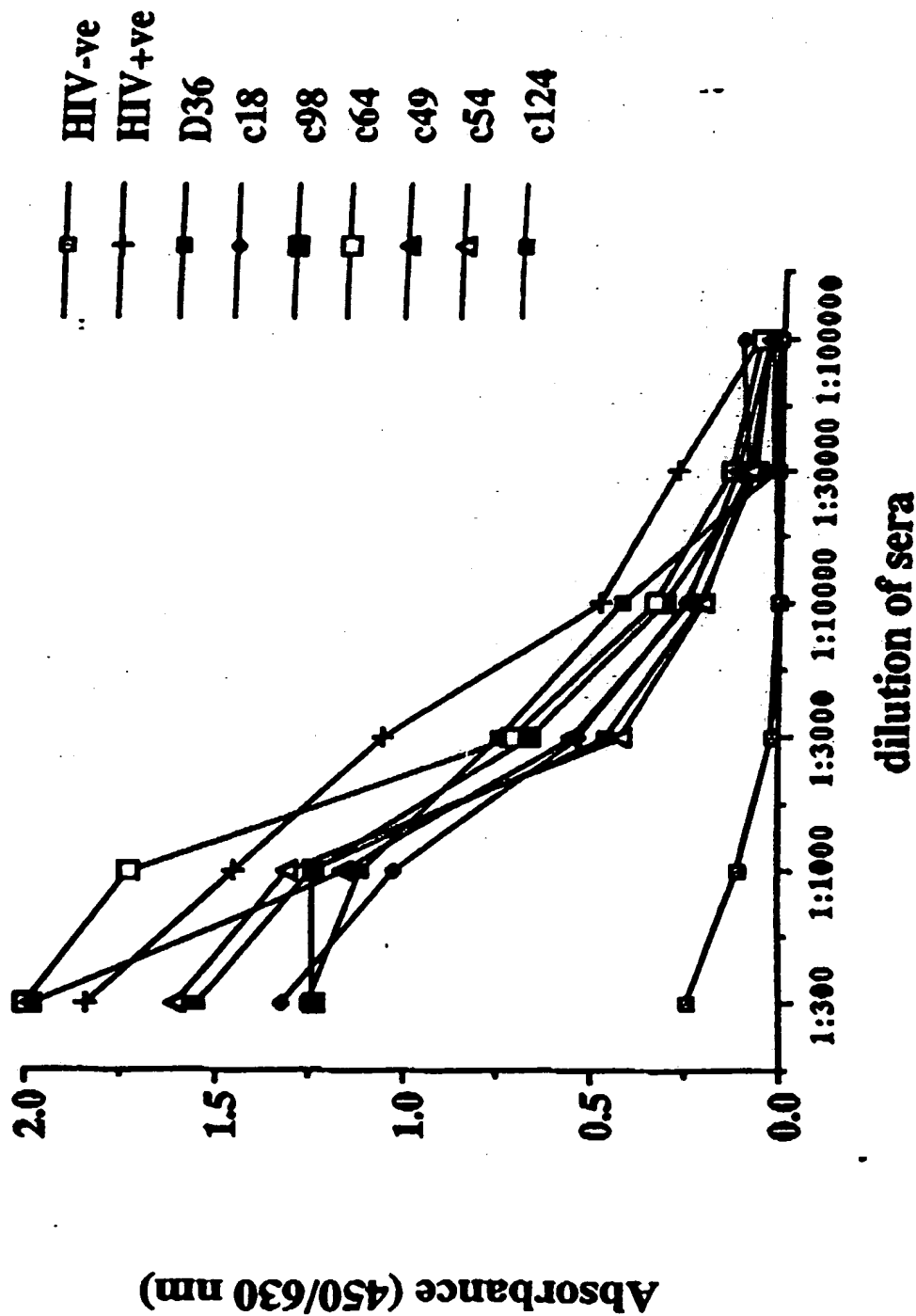


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FIGURE 13C (i)



Asymptomatic sera vs Nef aa20-36





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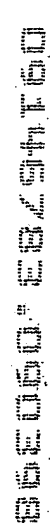
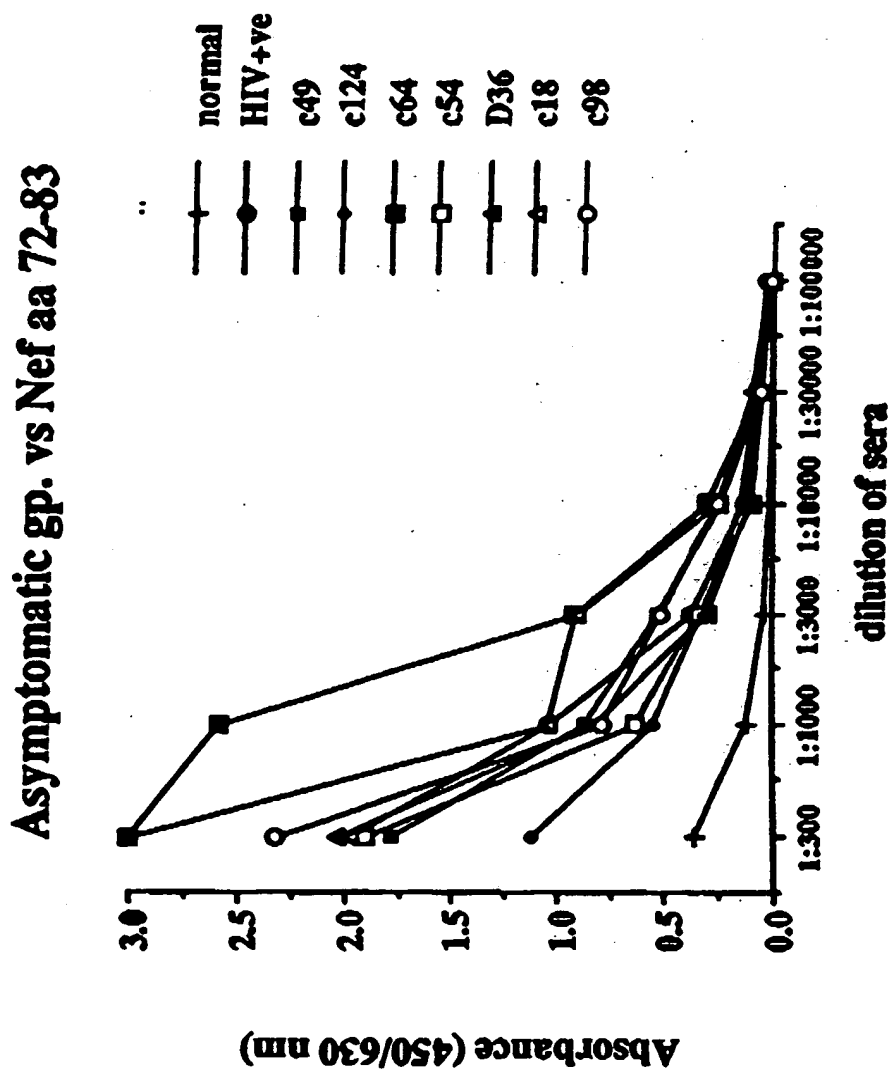
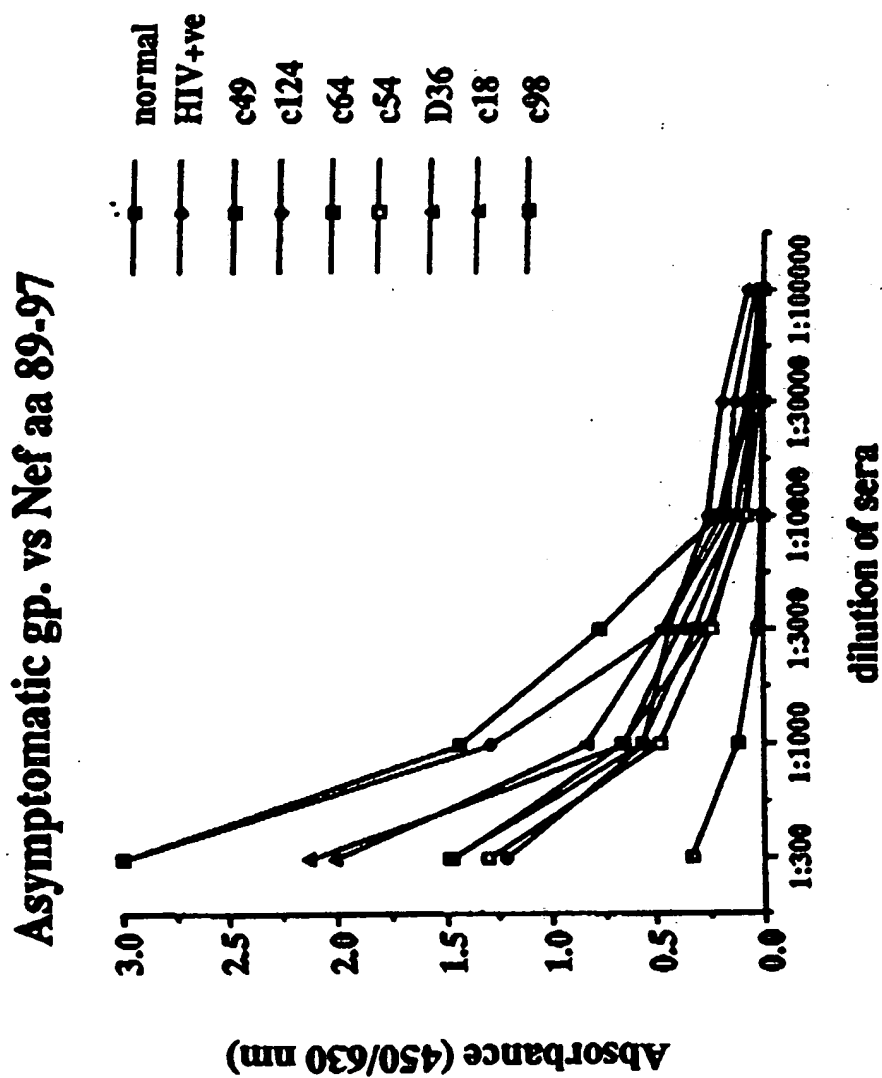


FIGURE 13C (iv)



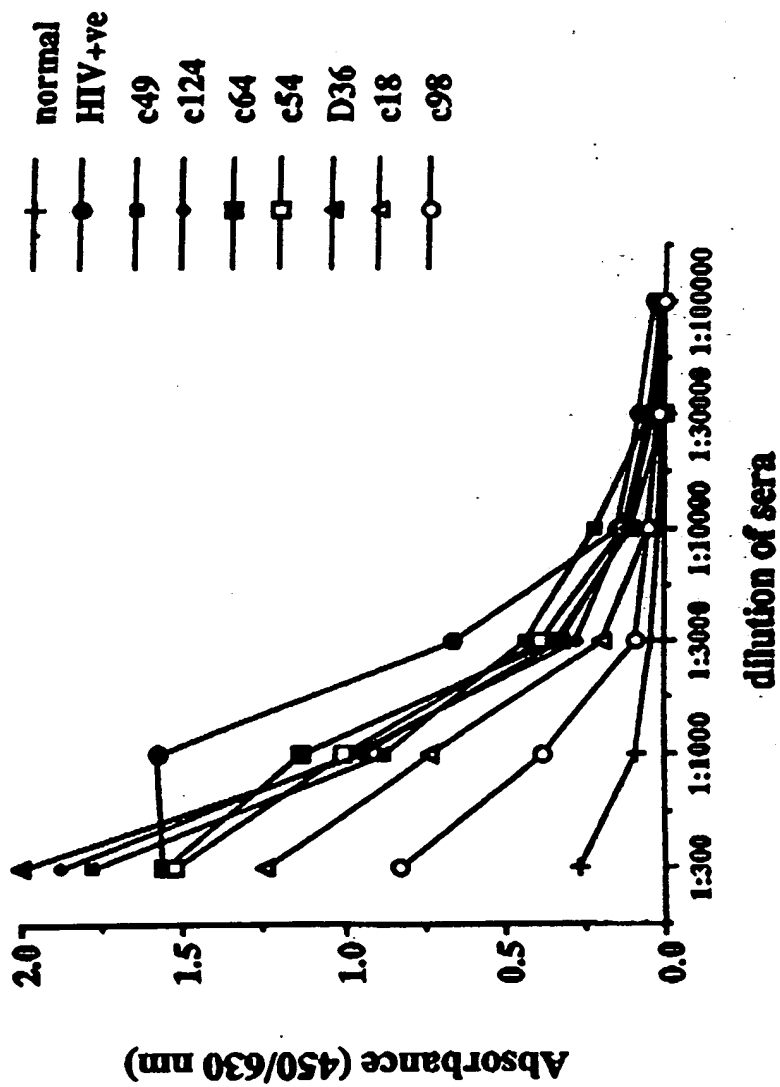
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FIGURE 13C (v)



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Asymptomatic gp. vs Nef aa 109-114



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FIGURE 13C (vii)

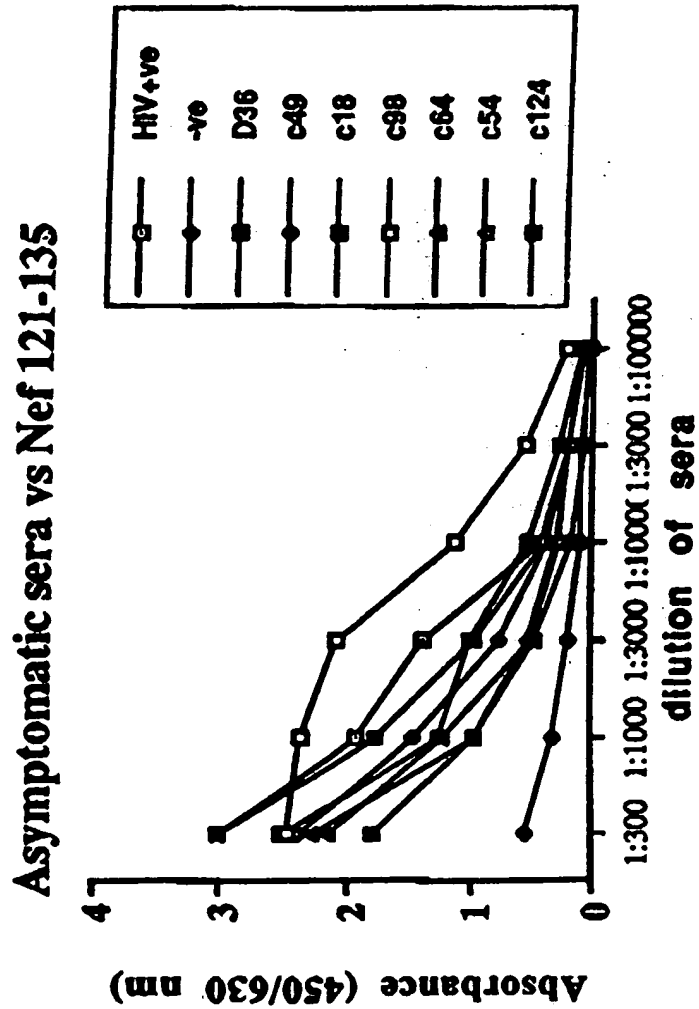
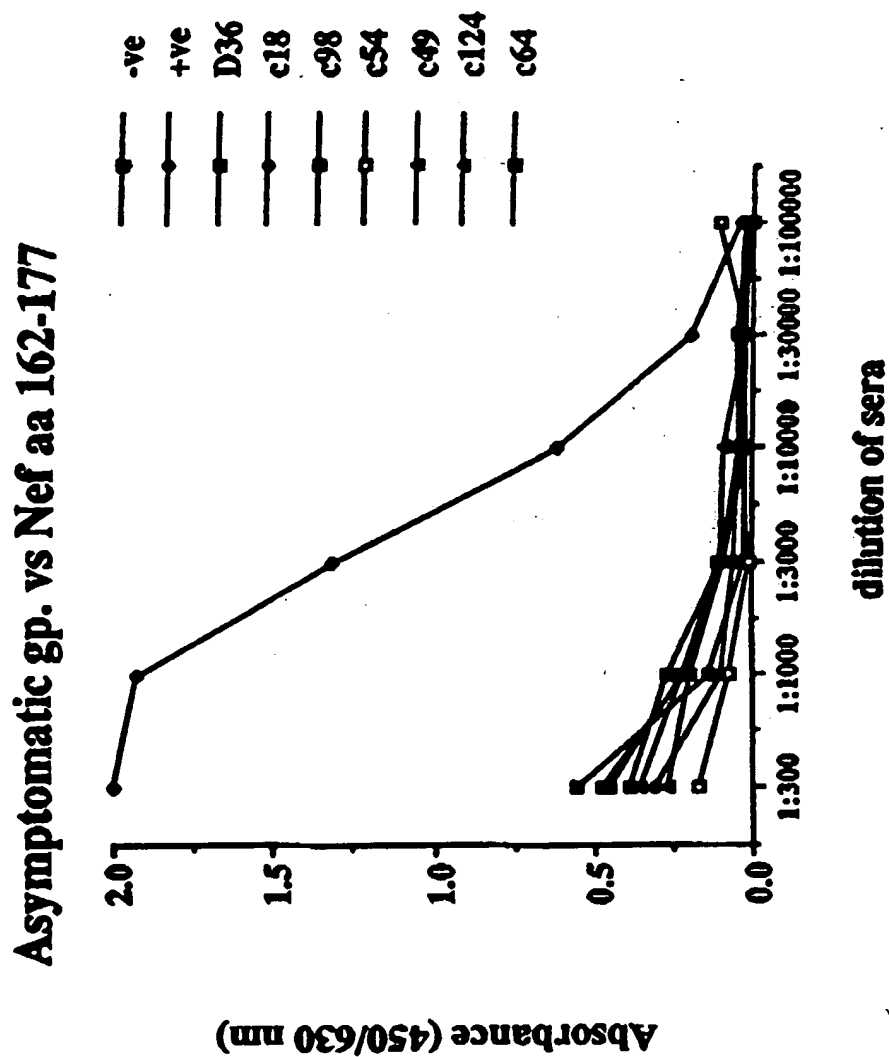


FIGURE 13C (viii)



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FIGURE 13C (ix)

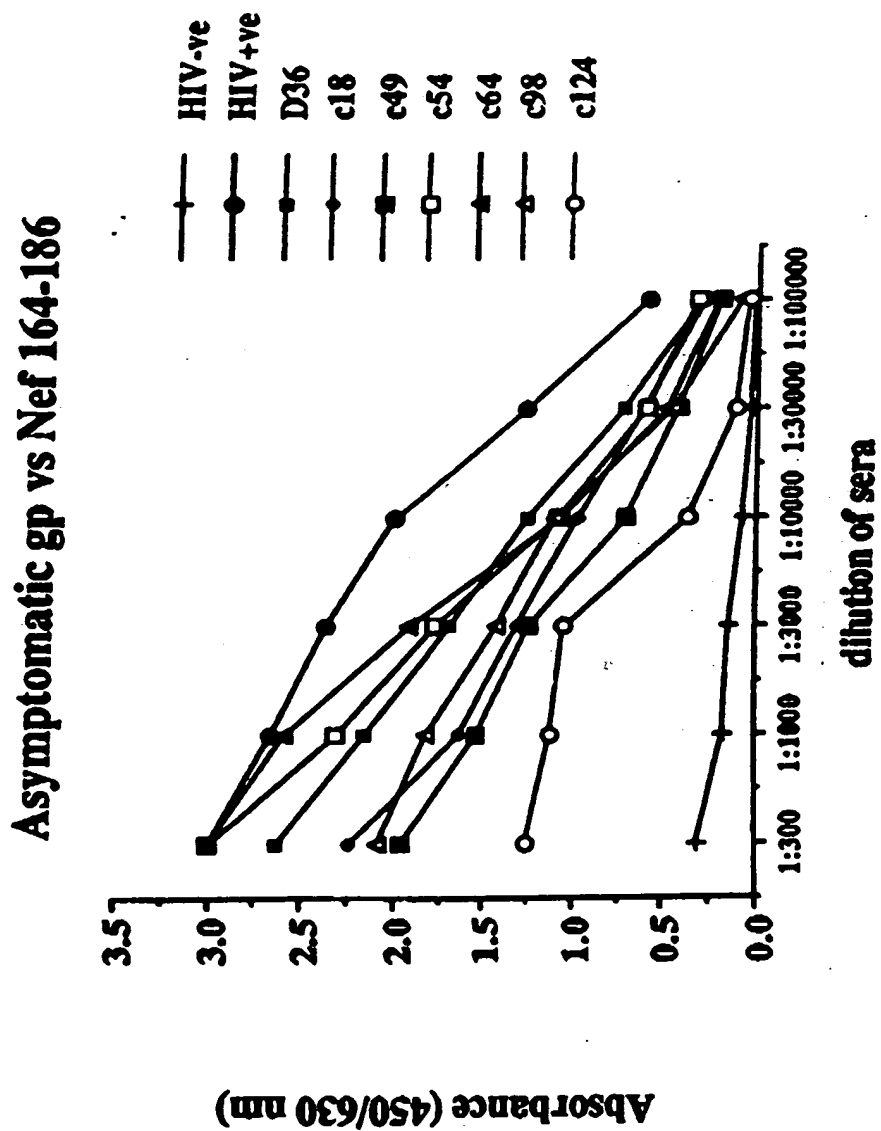
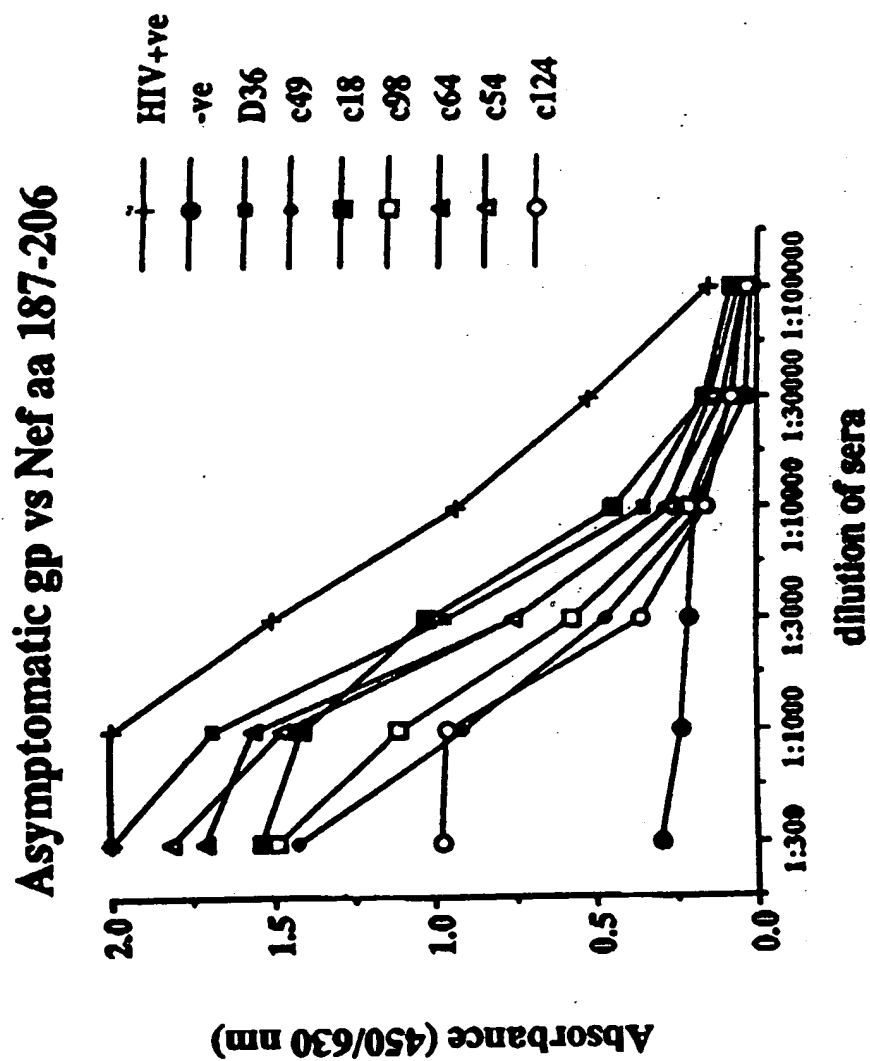
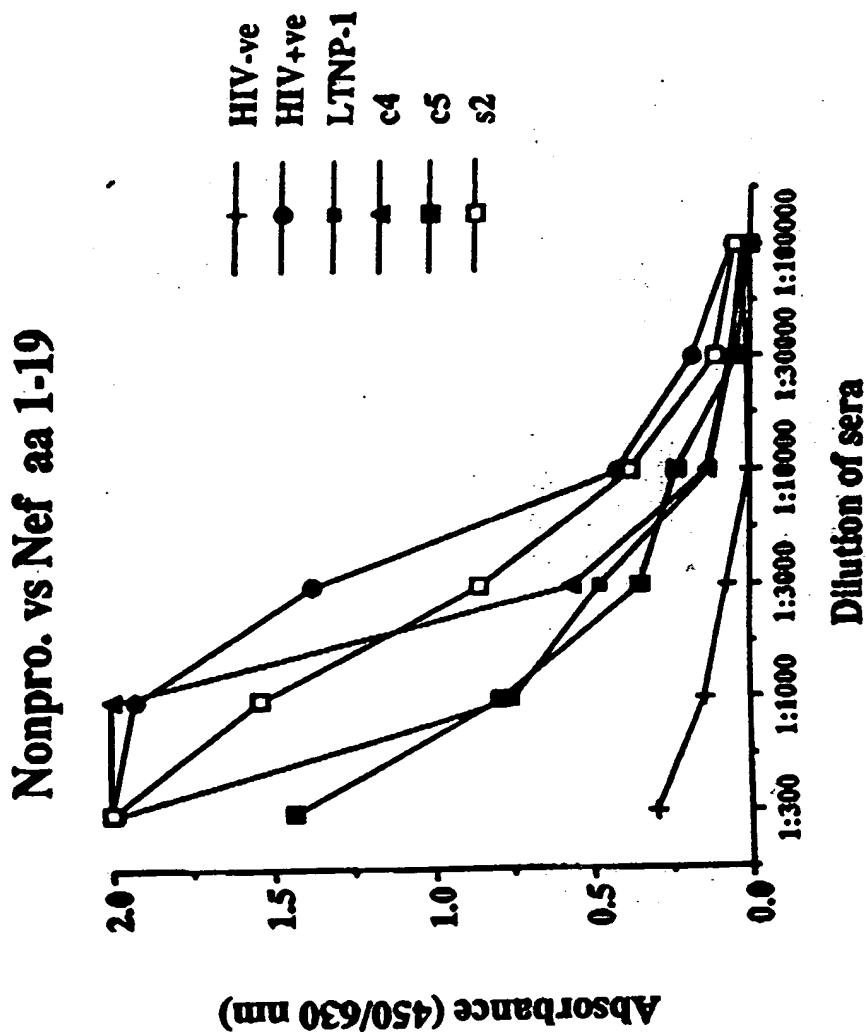


FIGURE 13C (x)

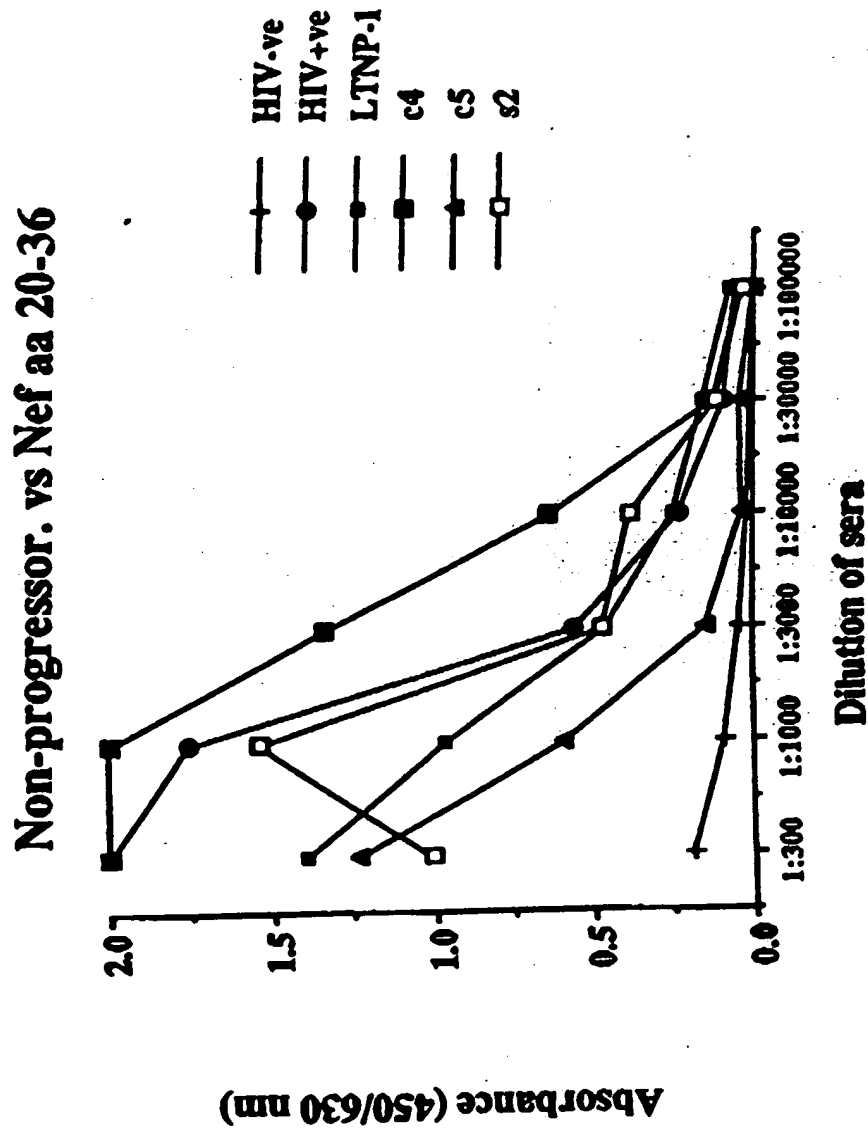


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FIGURE 13D (i)

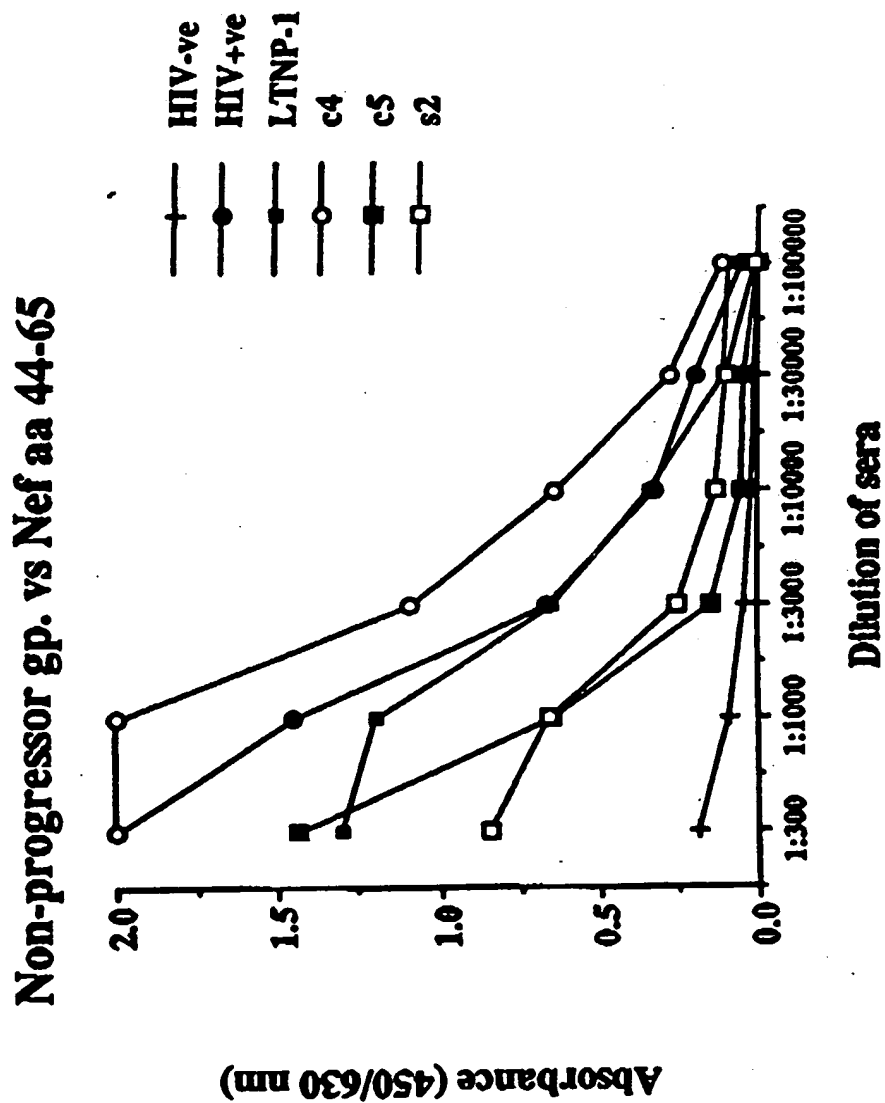


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FIGURE 13D (ii)



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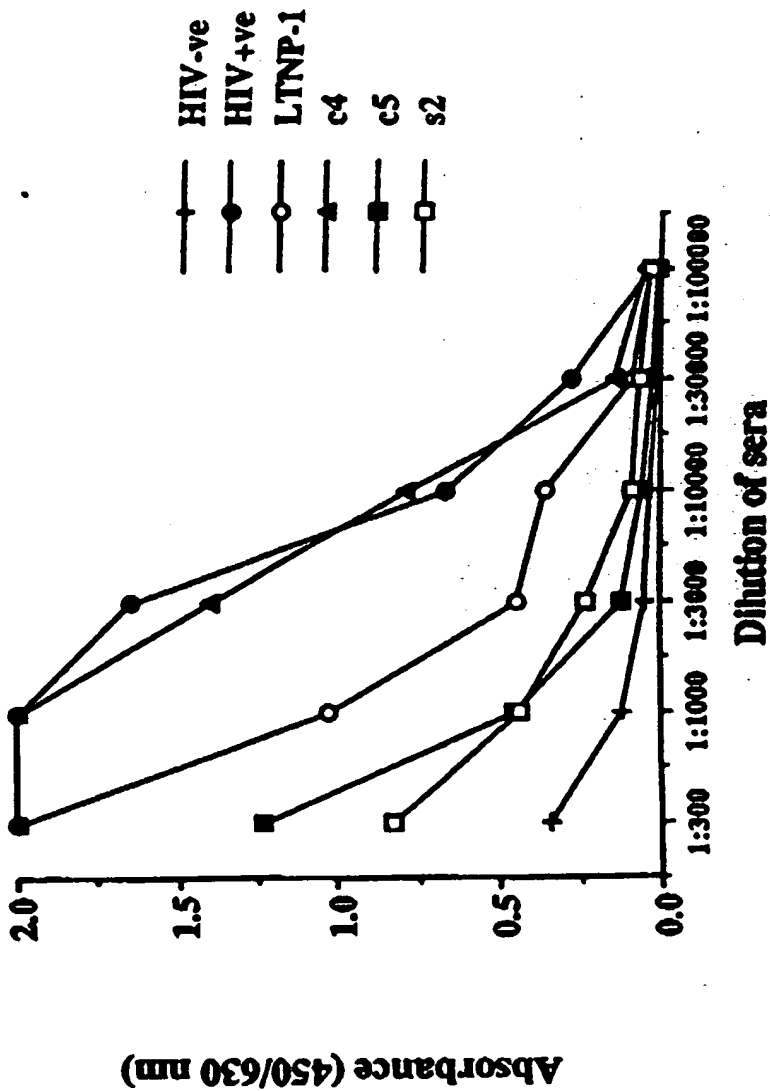
FIGURE 13D (iii)



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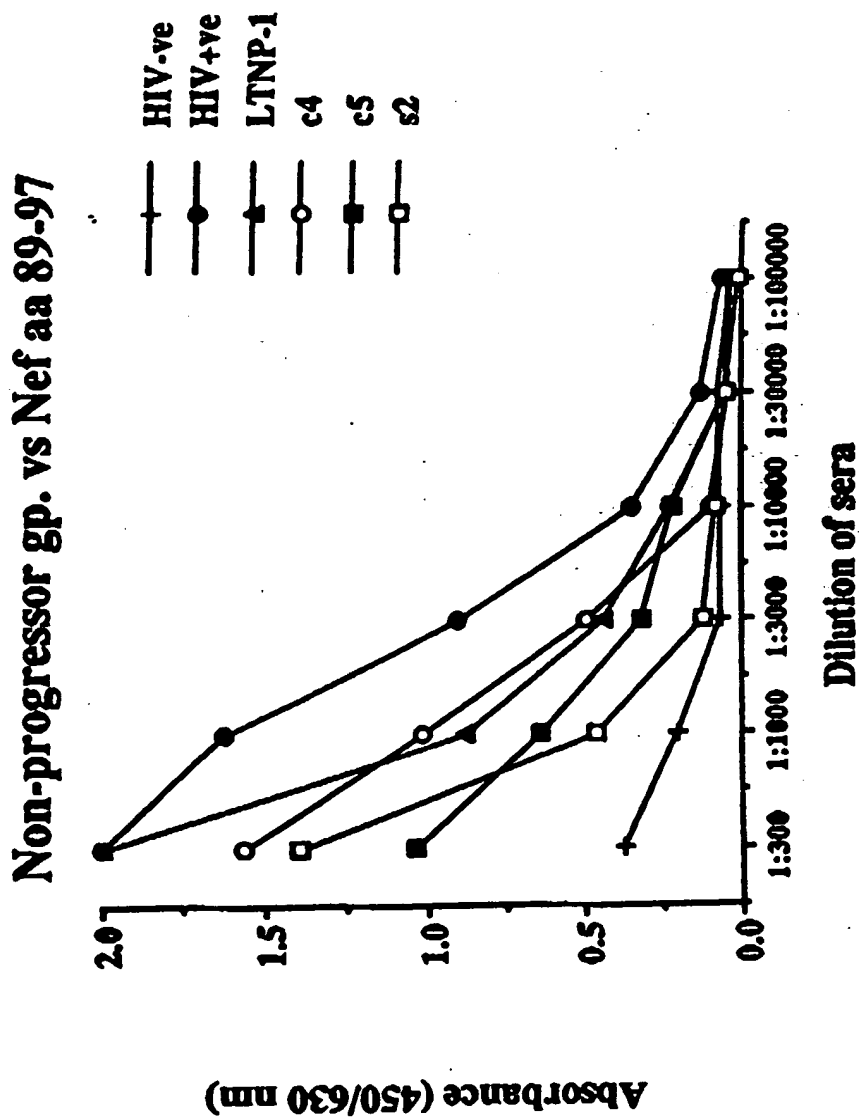
FIGURE 13D (iv)

Non-progressor gp. vs Nef aa 72-83



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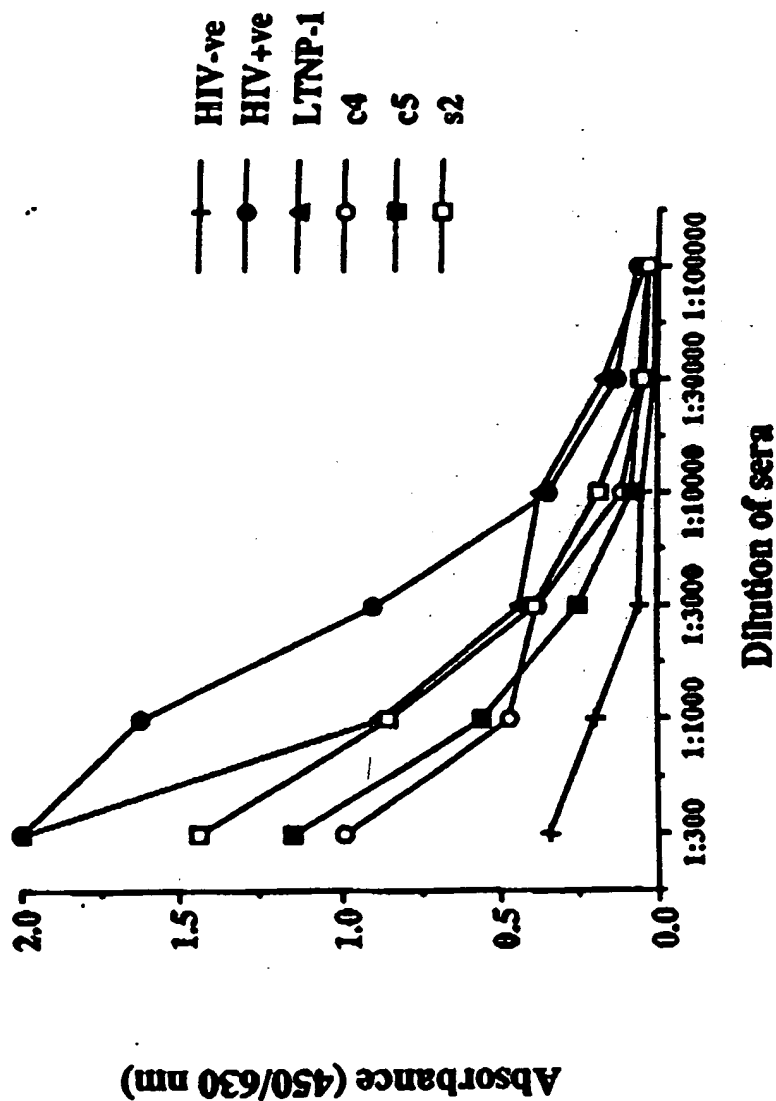
FIGURE 13D (N)



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FIGURE 13D (vi)

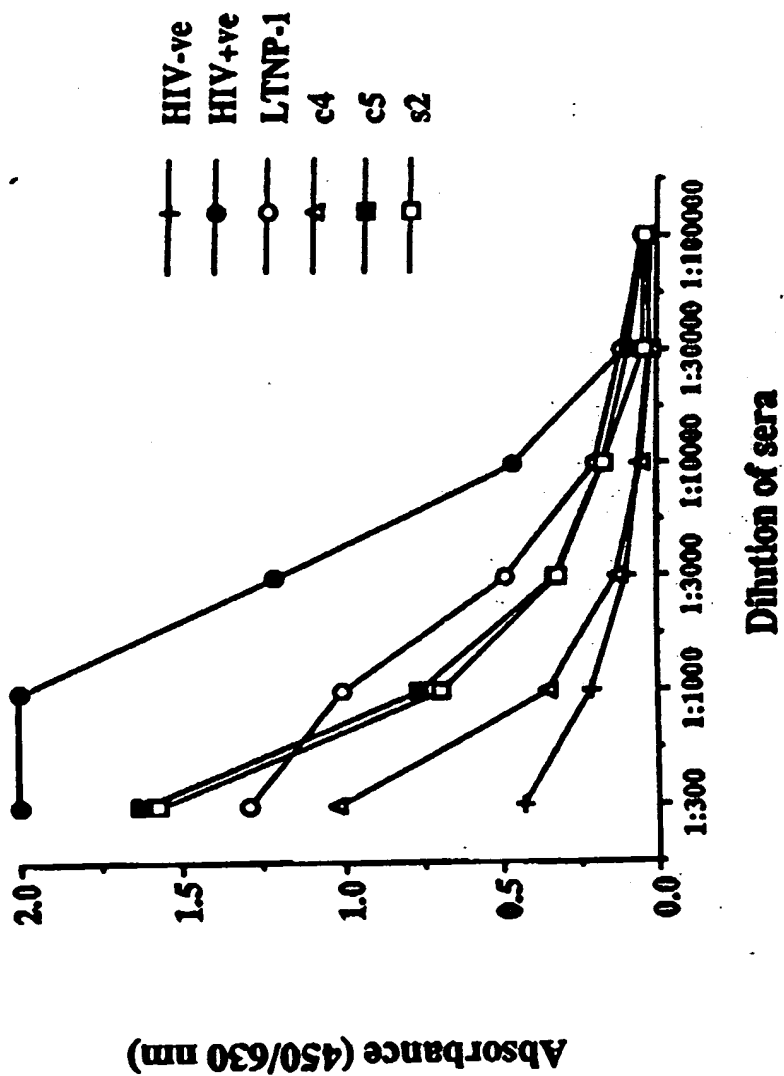
Non-progressor gp. vs Nef aa 109-114



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FIGURE 13D (viii)

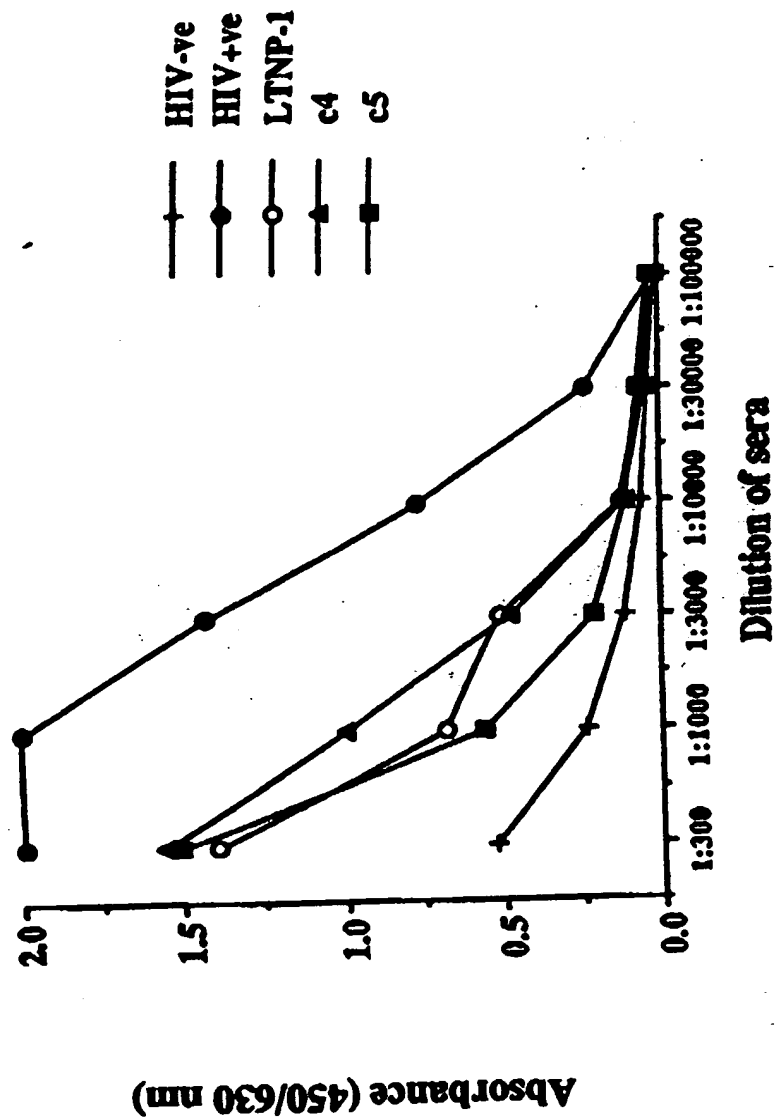
Non-progressor gp. vs Nef aa 121-135



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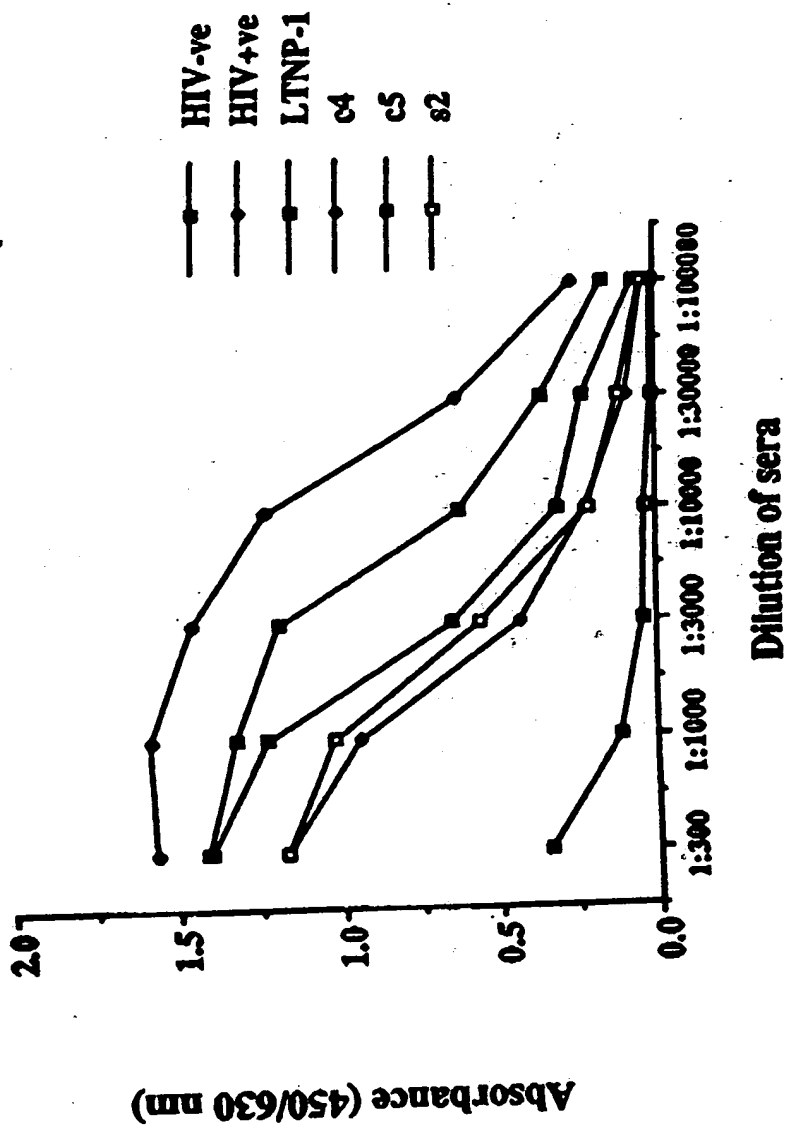
FIGURE 13D (viii)

Non-progressor gp. vs Nef aa 162-177



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FIGURE 13D (ix)

Non-progressor gp. vs Nef aa 164-186



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FIGURE 13D (x)

Non-progressor gp. vs Nef aa 187-206

